

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
(B) STRAIN: ATCC 9184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
10	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
	GTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
15	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GA CTCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
20	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
25	CGACGGTCTG	CG				812

2) INFORMATION FOR SEQ ID NO: 733

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
(B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

45	TGGTTGTTGC	TGCGACTGAC	GGYCCGATGC	CGCAGACCCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCTGGAAGT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
50	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	450
55	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCYGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTA	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
60	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCCG	750

GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 800
 GACGGTCTGC GTTT 814

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2) INFORMATION FOR SEQ ID NO: 734

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Virchow
- (B) STRAIN: ATCC 51955

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

GGCGCGATCC TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 25 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 30 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCGGT CGTGTAGAAC 400
 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
 35 CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCAATGGAC GACGGTCTGC GTTTCGCA 828
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2) INFORMATION FOR SEQ ID NO: 735

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Serratia grimesii*
- (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG 50
 60 TGAGCACATC CTGCTGGGTC GTCAGGTGG CGTTCCTTTC ATCATCGTAT 100

	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAACCTGGTA	150,
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTTCGTGGT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GAAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
5	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
10	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
	CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCTGA	TTCACCCAAT	800
15	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

35	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
	ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAGAGATGG	150
	AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	GTTTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
40	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
	CTCCAGAGAG	AGATACAGAT	AAACCATTTCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
45	CAAGCACCAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
	CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
	GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAT	TCTATTTTCAG	700
	AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
50	TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

2) INFORMATION FOR SEQ ID NO: 737

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

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10 GTCAACATGA TGGAGCTCAT CAACAACATC GCGAAGGAGC ACGGCGGTTA      50
   CTCCGTGTTT GCGGGCGTGG GCGAGCGTAC CCGTGAAGGG AACGACTTCT      100
   ACCACGAAAT GAAGGACTCG AACGTTCTCG ACAAGGTCGC GCTGGTGTAC      150
   GGCCAGATGA ACGAGCCGCC GGGCAACCGT CTGCGCGTGG CGCTGACGGG      200
   CCTCACGATG GCCGAGCACT TCCGTGACGA AGGCCTCGAC GTGCTGTTCT      250
15 TCGTCGACAA CATCTACCGT TTCACGCTGG CCGGTACCGA AGTGTGCGCG      300
   CTGCTCGGCC GTATGCCGTC GGCAGTGGGC TATCAGCCGA CGCTGGCTGA      350
   AGAAATGGGC AAGCTGCAAG AGCGCATCAC GTCGACGAAG AAGGGCTCGA      400
   TCACGTCGGT T                                     411

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2) INFORMATION FOR SEQ ID NO: 738

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium bifermentans*
(B) STRAIN: ATCC 638

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

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TACAAGAGCT TATTAACAAT ATAGCTACTC AACACGGTGG TATATCAGTA      50
TTCGCAGGTG TTGGAGAGAG AACAAAGAGAA GGTAACGACT TATTCATGA      100
40 GATGAGCGAT ACAGGAGTTA TAAATAAAAC AGCTCTAGTA TTCGACAAA      150
   TGAATGAGCC ACCTGGAGCA AGAATGAGAG TTGCTTTAAC TGGTCTTACA      200
   ATGGCTGAAT ACTTCAGAGA TCAACAAGGG CAAGACGTTT TATTATTCGT      250
   AGATAATATA TTCCGTTTCA CTCAAGCAGG ATCTGAGGTT TCTGCACTTC      300
   TTGGACGTAC TCCATCAGCA GTTGGATACC AACCAACATT AGCAACAGAG      350
45 ATGGGTAGAT TACAAGAGAG AATAACATCT ACAAATAAAG GGTC          394

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2) INFORMATION FOR SEQ ID NO: 739

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

	TTAATAAACA	ACATAGCTAA	ACAACATGGT	GGTTTATCAG	TATTTACTGG	50
	AGTTGGTGAA	AGATCAAGAG	AAGGTAATGA	CTTATATCAT	GAAATGAGAG	100
	AGTCAGGAGT	TATTGATAAG	ACAGCATTAG	TATTTGGACA	AATGAATGAG	150
10	CCACCGGGTG	CCAGAATGAG	AGTTGCATTA	ACAGGTCTTA	CTATGGCAGA	200
	GTATTTTAGA	GATAAAGGTC	AAGATGTGTT	ACTATTCATA	GATAACATAT	250
	TCAGATATAC	TCAAGCAGGT	TCAGAGGTTT	CAGCATTACT	TGGAAGAACA	300
	CCTTCAGCGG	TTGGATATCA	GCCAACACTT	GCAACTGAAA	TGGGTGCACT	350
	TCAGGAAAGA	ATTACATCAA	CAGTTAATGG	TTCTATTACG	TCAG	394

2) INFORMATION FOR SEQ ID NO: 740

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

	TTATAAACAA	TATTGCTAAG	CAACATGGTG	GTATTTCTGT	ATTTTCAGGA	50
35	GTAGGAGAAA	GAACAAGAGA	AGGTAACGAC	CTTTATGGCG	AAATGAGTGA	100
	GTCTGGAGTT	ATAAATAAAA	CAGCTCTAGT	ATTTGGTCAA	ATGAATGAAC	150
	CACCTGGAGC	GAGAATGAGA	GTTGCTTTAA	CTGGACTTAC	AATGGCAGAA	200
	CATTTTLAGAG	ATGAGCAAGG	ACAAGACGTT	TTACTTTTCG	TTGATAATAT	250
	ATTCCGTTTC	ACACAAGCTG	GTTCAGAAGT	TTCAGCACTT	CTAGGACGTA	300
40	TGCCATCAGC	TGTTGGTTAT	CAGCCAACAT	TAGCTACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATAACATC	AACTAAGAAA	GGTTCAATAA	CAT	393

45 2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium ramosum*
 (B) STRAIN: ATCC 25582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

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	TTGATTCAAG	AATTCATTAA	TAACATTGCT	ACAGAACATG	GTGGTTTATC	50
	AGTTTTTGCT	GGAGTTGGTG	AACGTAGCCG	TGAAGGTAAT	GATTTATATT	100
	ATGAAATGAA	GGAAAGTGGT	GTTTTATCTA	AAACAACACT	AGTATTTGGA	150
	CAGATGAATG	AACCCCCAGG	AGCTCGTTTA	AGAGTTGCTT	TAACGGGTCT	200
5	TACTATGGCA	GAAGAATTCC	GTGATGAACA	AGGTCAGGAT	GTCTTATTAT	250
	TCATCGATAA	TATTTTCCGT	TTTACTCAAG	CTGGATCTGA	AGTATCTGCC	300
	TTACTTGGAC	GGGTACCATC	ACAAGCTGGG	TATCAGCCAA	CTTTAGCAAC	350
	CGAAATGGGT	GCTTTACAAG	AACGGATTAC	ATCAACTAAA	AAAGGATC	398

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2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12964

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

	TAGCTAAGGA	ACACGGTGGA	CTTTCAGTAT	TCACAGGTGT	TGGAGAAAGA	50
	TCAAGAGAAG	GTAATGATTT	ATATTACGAA	ATGAAAGAAT	CAGGAGTTAT	100
30	AGACAAGACA	GCTCTAGTGT	TTGGACAAAT	GAATGAATCT	CCAGGAGCTA	150
	GAATGAGAGT	ATCTTTAACA	GGATTAACATA	TGGCTGAATA	TTTCAGAGAT	200
	CAAGGTCAAG	ATGTGCTTTT	ATTCATAGAT	AACATATTTA	GATTTACTCA	250
	AGCTGGATCA	GAAGTATCGG	CTTTACTTTG	AAGAATACCA	TCAGCAGTTG	300
	GTTATCAACC	AACACTAGCA	ACTGAAATGG	GTGCACTTCA	AGAAAGAATT	350
35	ACTTCAACTA	AAAATGGATC	AATAACTTCA			380

2) INFORMATION FOR SEQ ID NO: 743

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

55	TTAATAAATA	ATATAGCAAA	AGAGCATGGT	GGTCTTTCTG	TATTTACAGG	50
	AGTTGGAGAA	AGGTCAAGAG	AAGGTAACGA	CTTATATTAT	GAAATGAAAG	100
	AGTCAGGGGT	TATAGATAAG	ACAGCTTTAG	TATTTGGACA	AATGAATGAA	150
	TCACCAGGAG	CAAGAATGAG	AGTTTCATTA	ACTGGATTAA	CTATGGCTGA	200
	ATATTTTAGA	GATCAAGGTC	AAGACGTTCT	TTTATTTATA	GATAATATAT	250
60	TTAGATTTAC	TCAAGCGGGA	TCAGAAGTTT	CTGCGTTATT	AGGAAGAATT	300

CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGAGCACT 350
TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

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2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

TTCCCCCGCA CGCATGCCCA AGGTGTTCTGA TGCCCTGAAG CTCGACGGCT 50
CGGCCCTGAC GCTGGAAGTG CAGCAACTGC TGGGTGACGG CGTTGTGCGT 100
ACCATCGCCC TGGGTTTCGTG CGACGGTCTG CGTCGCGGCC TGATGGTGTGTC 150
25 CAACACCGGC AACCCCATCA CCGTGCCCGT GGGCAAGGCG ACGCTGGGTC 200
GCATCATGGA CGTGCTGGGC AATCCCATCG ACGAACGTGG TCCCGTGGAT 250
CAGGCGCTGA CGGCTCCCAT CCACCGCAAG GCACCGGCTT ATGACGAGCT 300
GTCGCCTTCG CAGGAACTGC TGGAAACCGG CATCAAGGTG ATCGACCTGA 350
TCTCGCCCTT CGCCAAGGGC GGCAAGGTGG GTCTGTTTCG TGCGGCCGGT 400
30 GTGGGCAAGA CCGTGAACAT GATGGAATC ATCAACAACA TCGCCAAGGG 450
CCACGGTGGT CTGTCGGTGT TCGCCGGTGT GGGTGAACGT ACCCGCGAAG 500
GCAATGACTT CTATCACGAA ATGTCGGACG CCGGCGTGGT CAACCAGGAG 550
TCGCTGAACG ACTCCAAGGT GGCCATGGTC TACGGCCAGA TGAACGAACC 600
CCCGGGCAAC CGTCTGCGCG TGGCGCTGAC CGGCCTGACC ATGGCCGAAG 650
35 CCTTCCGTGA CGAAGGCAAG GACGTGCTGT TCTTCGTGGA CAACATCTAC 700
CGCTACACGC TGGCCGGTAC CGAAGTGTCC GCTCTGCTGG GTCGCATGCC 750
TTCCGCCGTG GGCTACCAGC CCACGCTGGC CGAGGAAATG GGCCGCCTGC 800
AAGAGCGCAT CACCTCGACC AAGGTCGGTT CGATCACTTC CAC 843

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2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
55 (B) STRAIN: ATCC 13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

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GCCGTACCAC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT 50
TCTGGTGCTG GAAGTTCAGC AGCAGCTGGG CGGCGGTATC GTACGTACCA 100

	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGTTTGACAT	GAAAGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTCGGCGGT	GCGGGTGTAG	400
	GTAAAACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCGCCCG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
15	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Neisseria canis*
- (B) STRAIN: ATCC 14687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

35	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCT	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGGCG	GTAGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
40	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTG	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
45	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCGG	TAACCGTTTG	CGCGTTGCGC	600
	TAACTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
50	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

55 2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cinerea*

(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

10 CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG 50
 TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA 100
 TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT 150
 ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCGTAT 200
 15 TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATACCG 250
 ACAAAAGCCG TGCCATTCAC CAAACTGCTC CGAAATTCTGA CGAGTTGTCT 300
 TCAGCTACCG AATTGTTGGA AACCGGTATT AAAGTGATCG ACTTGCTGTG 350
 TCCGTTTGCT AAAGGCGGTA AAGTAGGTCT GTTCGGTGGT GCCGGTGTGG 400
 GCAAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC 450
 20 AGCGGTCTGT CCGTGTTCGC AGGTGTGGGT GAGCGTACCC GTGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA 550
 TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT 600
 TTGACCGGTT TGA CTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
 CGGTAAAGGC CGCGACGTAT TGTTCTTCGT TGACAACATC TACCGTTACA 700
 25 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
 GTGGGTTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
 TATTACCTCT ACCCAAACCG GTTCCATTAC T 831

30

2) INFORMATION FOR SEQ ID NO: 748

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cuniculi*

(B) STRAIN: ATCC 14688

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG 50
 AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 50 CTCTGGTGCA CCGATTTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAAC TCAACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTCCGGTGG TGCAGGTGTG 400
 55 GGTAAAACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 ACGATTTTTA TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC 550
 TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTCAGATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTTG CATTGACAGG CTTGACGATG GCAGAAATATT 650
 60 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG 700

TTCGTTGATA	ACATCTATCG	TTACACACTG	GCTGGTACGG	AAGTGT ² AGC	750'
ACTTCTAGGT	CGTATGCCAT	CAGCAGTAGG	TTATCAACCG	ACTCTGGCTG	800
AAGAAATGGG	TGCGTTGCAA	GAGCGTATTA	CCTCAACGCA	ATCGGGTTCG	850
ATCACTTTCG	GG				862

5

2) INFORMATION FOR SEQ ID NO: 749

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
- (B) STRAIN: ATCC 25295

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

25	GGA	ACT	CCCA	CGT	GAC	GCTA	TCC	CGC	ATGT	TTT	TGAT	GCA	TTA	AAAT	TTAG	50		
	TTG	AAA	ATGA	CCT	AAC	CTTA	GA	AGT	TCA	AC	AACT	TTT	GGG	GG	ATG	GTGTA	100	
	GTG	CGT	ACCA	TTG	CGA	TGGG	TAG	TT	CAG	AT	GG	ATT	AA	AGC	GTG	TATGGC	150	
	TGT	GA	ATAAT	ACC	GG	A	CTC	CG	ATT	ACT	GT	TC	CT	GTT	TGGC	CGT	GAACTT	200
	TGG	GT	CGTAT	CAT	GG	ATGTA	TTG	GGT	TA	ATC	CG	GT	TG	ATGA	GGC	AGGTCCG	250	
	GT	AA	ATGCAT	CCA	ATA	CACG	TG	CG	ATCC	AT	CA	AG	AGG	CTC	CTA	AGTTTGA	300	
30	TG	AG	CTTTCT	TCA	ACA	ACCG	AAT	TAT	TAGA	AA	CT	GGC	ATT	AAG	GT	TATCG	350	
	ACT	TG	TTATG	TCC	GTT	TGCC	AA	AGG	TGGTA	AAG	TAG	GTCT	GTT	TG	TGGT	GGT	400	
	GCG	GGT	GTAG	GT	AAA	ACCGT	AA	TAT	GATG	GAG	TTA	ATTA	ACA	AC	ATTGC		450	
	CA	AGG	CACAT	AG	CGG	TTTGT	CT	GTG	TTTGC	AGG	CGT	GGGT	GA	ACG	TACTC		500	
	GT	GA	AGGTAA	TG	ACT	TCTAT	CAC	GAG	ATGA	AAG	ATT	CCAA	CG	TAT	TGGAC		550	
35	AA	AGT	TGGCAA	TGG	TTT	TACGG	TC	AG	ATGAAC	GA	ACC	TCCAG	GCA	ACC	GTCT		600	
	GCG	CGT	TGCT	TTG	ACC	GGTT	TG	ACT	ATGGC	CGA	ATA	CTTC	CGT	GAC	GAAA		650	
	AAG	ACG	AAAA	CGG	TAA	AGGT	CG	C	GACGTAT	TG	TTCT	TCGT	GG	ACA	ACATT		700	
	TAC	CGT	TACA	CTT	TG	CCGG	TAC	GGA	AGTA	TCC	GC	ATTGC	TGG	GT	TCGTAT		750	
	GC	CTT	CAGCA	GTA	GGT	TACC	AAC	CG	ACATT	GG	CTGA	AAGAA	AT	GGG	TCGTT		800	
40	TG	CA	AAGAGCG	TAT	TAC	CTCT	ACC	CAG	ACAG	GCT	CTAT	TAC	TT	CC			844	

2) INFORMATION FOR SEQ ID NO: 750

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
- (B) STRAIN: ATCC 13120

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

60	CGCGACGCTA	TTCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
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	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
5	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCTGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTTCGC	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
10	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	GGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
15	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

20 2) INFORMATION FOR SEQ ID NO: 751

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 31426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

35	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTCGC	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
40	TGTCGATGTA	TTGGGAACCTC	CTGTTGACGA	GGCAGGTCCA	ATTGATACCG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGGTCT	GTTCGGCGGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCAAACCG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 60 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
(B) STRAIN: ATCC 27628

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCGG	CATGACTGTG	AGCAATACTG	150
15	GTTCGCCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGTCTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTC	GGCGGTGCCG	GTGTGGGTAA	400
20	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCCGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCAA	CCGTCTGCGC	GTGCTTTGA	600
	CCGGTTTGAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
25	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTC	CATTA			825

30

2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
(B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

	GATGCGATTG	CGCATGTTTA	CGATGCCCTG	AAATTGGACG	AGAACGGTCT	50
	GACCCCTGGA	GTCCAACAGC	TTTTTGGGTG	CGGCGTTGTC	CGTACTATTG	100
50	CAATGGGTTAG	TTCAGACGGC	CTGAAACGCG	GCATGTCTGT	CAGCAATACC	150
	GGTGCGCCAA	TCACTGTGCC	GGTAGGTAAA	GGTACGTTGG	GCCGTATTGT	200
	CGACGTATTG	GGTACACCTG	TTGACGAAGC	AGGTCCGATC	GATACCGACA	250
	AGAGCCGCGC	CATCCACCAA	ACCGCCCCGA	AATTCGACGA	GTTGTCTTCA	300
	ACTACCGAAT	TGTTGGAAAC	CGGCATTAAA	GTGATCGATT	TGCTGTGTCC	350
55	GTTTGCTAAG	GGCGGTAAAG	TAGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	400
	AAACCGTGAA	CATGATGGAA	TTGATCAACA	ACATCGCCAA	AGCGCACAGC	450
	GGTCTGTCCG	TGTTTGACAG	CGTGGGCGAG	CGTACCCGCG	AAGGTAACGA	500
	CTTCTACCAC	GAGATGAAAG	ATTCCAACGT	ATTGGATAAA	GTAGCCATGG	550
	TGTATGGTCA	GATGAACGAA	CCTCCGGGCA	ACCGTCTGCG	CGTTGCTTTG	600
60	ACCGGTTTGA	CGATGGCCGA	ATACTTCCGC	GACGAAAAAG	ACGAAAACGG	650

CAAAGGCCGC	GACGTATTGT	TCTTCGTGGA	CAACATCTAC	CGTTACACCC	700
TGGCCGGTAC	CGAAGTATCC	GCACTGTTGG	GCCGTATGCC	TTCCGCAGTG	750
GGTTACCAAC	CGACATTGGC	TGAAGAAATG	GGTCGTTTGC	AAGAGCGTAT	800
TACCTCTACC	CAAACCGGTT	CCATTACTTC	C		831

5

2) INFORMATION FOR SEQ ID NO: 754

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 2241C

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	GTAGTCCGTA	100
CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	GACTGTGAGC	150
AATACCGGTG	CGCCATTAC	TGTGCCGGTA	GGTAAAGGTA	CGTTGGGACG	200
CATTGTTCGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	CCAATCGATA	250
CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	TGACGAACTG	300
TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	TTGACTTGCT	350
GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGC	GGTGCCGGTG	400
TGGGTAA AAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	CGCCAAAGCG	450
CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	CCCGCGAAGG	500
TAACGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GATAAAGTGG	550
CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	TTTGCGCGTC	600
GCATTGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	AAAAAGACGA	650
AAACGGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGAACAAC	ATCTACCGTT	700
AACTCTAGC	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	TATGCCGTCT	750
GCAGTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	GTTTGCAGGA	800
GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC		836

45

2) INFORMATION FOR SEQ ID NO: 755

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
------------	------------	------------	------------	------------	----

430

	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	GTAGTTCGTA	400
	CTATTGCAAT	GGGTAGTTCG	GATGGTTTGA	AACGCGGCAT	GACTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTTCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
5	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
10	TAATGACTTC	TACCACGAGA	TGAAAGATTG	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCG	TATGCCTTCA	750
15	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

20 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

35	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
40	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAAGTCTC	CGAAATTCTGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 60 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

	CCCGTGATGC	TATTCCCATG	TATACGATGC	CCTGAAATTG	GTAGATAACG	50
	ATCTGACCCT	GGAAGTGCAA	CAACTTTTAG	GTGATGGTGT	GGTTCGTACC	100
	ATTGCAATGG	GTAGTTCAGA	CGGCCTAAAA	CGTGGTATGG	CTGTTAACAA	150
15	TACCGGCGCT	CCGATTACTG	TTCCGGTGCG	GAAAGCCACC	TTGGGACGTA	200
	TTATGGATGT	GTTGGGTAAT	CCGGTTGATG	AAGCAGGTCC	TGTTGTATCA	250
	GAAGAAACTC	GCGCTATTCA	TCAAGCTGCC	CCTAAATTTG	ACGAACTGTC	300
	TTCAGCAACT	GAGTTGTTGG	AAACAGGCAT	TAAAGTAATT	GACTTGCTGT	350
	GCCCGTTTGC	CAAAGGTGGT	AAAGTAGGTT	TGTTTGGTGG	TGCCGGCGTG	400
20	GGTAAAACCG	TAAATATGAT	GGAGTTGATC	AACAACATCG	CGAAGGCACA	450
	TAGTGGTTTG	TCTGTATTTC	CCGGTGTAGG	TGAGCGTACC	CGTGAAGGTA	500
	ACGACTTCTA	CCATGAAATG	AAAGACTCTA	ACGTATTGGA	TAAAGTAGCC	550
	ATGGTTTATG	GCCAGATGAA	TGAACCTCCG	GGTAACCGTT	TGCGCGTTGC	600
	TTTGACTGGT	TTGACTATGG	CCGAATATTT	CCGTGACGAG	AAAGATGAAA	650
25	ACGGCAAAGG	TCGTGACGTC	TTGTTCTTTG	TGGATAATAT	CTATCGCTAT	700
	ACTCTGGCCG	GTAAGTGAAGT	GTCTGCACTG	TTAGGTCGTA	TGCCGTCTGC	750
	AGTAGGTTAT	CAGCCTACAT	TGGCAGAAGA	AATGGGTCGC	TTGCAGGAGC	800
	GTATTACTTC	TACTCAAACA	GGTTCGATTA	CTT		833

30

2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria animalis*
(B) STRAIN: ATCC 19573

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

	CGCGATGCCA	TTCCTCACGT	TTACGATGCC	CTGAAATTGG	ACGACACCGG	50
	TCTGACTTTG	GAAGTACAAC	AACTTCTGGG	CGACGGTGTG	GTACGTACCA	100
50	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GGGGTTTGTC	TGTGAGCAAT	150
	ACCGGTTCTC	CGATTGCCGT	TCCTGTCCGT	AAAGCGACTT	TGGGTCGTAT	200
	TATGGACGTA	TTGGGCAATC	CGGTTGATGA	AGCCGGTCCG	GTTGCTACCG	250
	AAGAGAAACG	TGCTATTAC	CAAGCCGCAC	CGAAGTTTGA	TGAATTGTCA	300
	TCAGCTACCG	AGTTGTTGGA	AACCGGTATT	AAAGTAATCG	ACTTGCTGTG	350
55	TCCGTTTGCA	AAAGGCGGTA	AAGTAGGTCT	GTTCGGCGGT	GCCGTTGTGG	400
	GCAAAACCGT	AAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCACAC	450
	AGCGGTCTGT	CTGTGTTTGC	CGGTGTAGGT	GAACGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTGTTGGAT	AAAGTAGCCA	550
	TGGTGTACGG	TCAGATGAAT	GAGCCGCCGG	GCAACCGCTT	GCGCGTGGCT	600
60	TTGACCGGCC	TGACTATGGC	CGAATACTTC	GTGACGAAAA	AGACGAAAAC	650

GGCAAAGGTC	GTGACGTATT	GTTCTTCGTG	GACAACATTT	ACCGCTACAC	700
ACTGGCCGGT	ACCGAAGTAT	CAGCATTGTT	GGGCCGTATG	CCGTCTGCAG	750
TAGGTTATCA	GCCGACATTG	GCAGAGGAAA	TGGGTCGCTT	GCAAGAGCGT	800
ATTACCTCTA	CCCAAACCGG	TTCGATTACC	TCT		833

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2) INFORMATION FOR SEQ ID NO: 759

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
25 ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTCGTTGTA	100
TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
AAGAACGTTG	GTCTATTTCAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
30 AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
TCCGTTTGCT	AAAGGTGGTA	AAGTAGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
GTAAAACAGT	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
TCAGGTTACT	CTGTATTTGC	TGGTGTGGT	GAGCGTACTC	GTGAGGGTAA	500
CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCCTTGAC	AAAGTATCGT	550
35 TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCAACA	750
TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAC	800
40 AGGTTCAATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CAGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGTGTGTC	GTCGATAACA	TCTATCGTTA	CACCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

20

2) INFORMATION FOR SEQ ID NO: 761

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
- (B) STRAIN: KIM D27

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
40	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCGGG	TGTAGGTAAA	400
45	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGGTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTACTGC	650
50	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

55

2) INFORMATION FOR SEQ ID NO: 762

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 408 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
- (B) STRAIN: GB8

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

	CGACGTGATC	GAGCCCTTCT	TCGTCGACGT	GATGCGCTCT	TGCAGCTTGC	50
	CCATTTCTTC	AGCCAGCGTC	GGCTGATAGC	CCACTGCCGA	CGGCATACGG	100
15	CCGAGCAGCG	CCGACACTTC	GGTACCGGCC	AGCGTGAAAC	GGTAGATGTT	150
	GTCGACGAAG	AACAGCACGT	CGAGGCCTTC	GTCACGGAAG	TGCTCGGCCA	200
	TCGTGAGGCC	CGTCAGCGCC	ACGCGCAGAC	GGTTGCCCGG	CGGCTCGTTC	250
	ATCTGGCCGT	ACACCAGCGC	GACCTTGTCG	AGAACGTTCG	AGTCCTTCAT	300
	TTCGTGGTAG	AAGTCGTTCC	CTTCACGGGT	ACGCTCGCCC	ACGCCC GCGA	350
20	ACACGGAGTA	ACCGCCGTGC	TCCTTCGCGA	TGTTGTTGAT	GAGCTCCATC	400
	ATGTTGAC					408

25 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium sordellii*
- (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

40	GAACTTATAA	ACAACATAGC	TACTCAACAT	GGTGGTATAT	CAGTATTCGC	50
	AGGTGTTGGA	GAGAGAACAA	GAGAAGGTAA	CGACCTTTAC	GGAGAAATGA	100
	GTGAGTCTGG	AGTTATAAAC	AAGACAGCTC	TAGTATTCGG	ACAAATGAAT	150
	GAGCCACCTG	GAGCAAGAAT	GAGAGTTGCT	TTAACTGGTC	TTACAATGGC	200
45	TGAATATTTT	AGAGATCAAG	AAGGACAAGA	CGTTTTATTA	TTCGTAGATA	250
	ATATATTCCG	TTTCACTCAA	GCAGGATCTG	AGGTTTCTGC	ACTTCTTGGA	300
	CGTACTCCAT	CAGCAGTTGG	ATACCAACCA	ACATTAGCTA	CAGAGATGGG	350
	TAGATTACAA	GAGAGAATAA	CATCTACAAA	TAAAGGGTCT	ATAACATCAG	400

50

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 405 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

435

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
 (B) STRAIN: ATCC 19402

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

	TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
	TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
10	ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
	TAGACAACAT	ATTTAGATTTC	ACTCAAGCAG	GTTTCAGAGGT	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
15	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
	CATCA					405

20 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

35	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
40	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATTA	CTTGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

45

2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 399 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium histolyticum*
 (B) STRAIN: ATCC 19401

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
5	GAAAGATTCT	GGGGTTATAG	AGAAAACTGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	GTACTTTTAT	TTATAGATAA	250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
10	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

30	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTCCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTCGTC	250
35	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

40

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 953 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAAACGTC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
60	GCTGATGCTC	CCGAGTTCGT	TGATCAATCC	CCCACTCCCG	AGATTCTCGA	200

	GACTGGTATC	AAGGTTGTCG	ATTTGCTTGC	TCCCTATGCT	CGTGGTGGTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTGC	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTTACT	CTATCTTCTG	350
	TGGTGTTCGGT	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
5	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCGTG	TTGCCTTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAGTG	600
	TCCGCTTTGC	TTGGTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
10	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700
	GTTCCATTAC	CTCCGTGCAA	GCTGTCTACG	TCCCTGCTGA	CGATTGACT	750
	GATCCTGCTC	CTGCTACTAC	TTTTGCTCAC	TTGGACGCCA	CCACTGTGTT	800
	GTCTCGTTCC	ATTGCTGAGT	TGGGTATCTA	CCCTGCTGTC	GATCCCCTTG	850
	ACTCCAAGTC	CCGTATCTTG	GATCCCCGTA	TCGTTGGTGA	TGAGCACTAC	900
15	TCTGTTGCCA	CTGGTGTCCA	ACAAATCCTT	CAAACTACA	AGTCGCTTCA	950
	AGA					953

20 2) INFORMATION FOR SEQ ID NO: 769

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

35	CGCGGTTCCA	AGGCCACCGA	CACCGGTGCC	CCCATCAAGA	TTCCCGTTGG	50
	TCACGGTACC	CTTGGTCGTA	TCATGAACGT	CACTGGTGAC	CCCATTGACG	100
	AGCGTGGTCC	CATCAAGGCC	ACCAAGTACG	CTCCCATCCA	CGCCGACCCC	150
	CCGGAGTTCA	CCGAGCAATC	CACCTCCGCT	GAGGTCCTCG	TTACCGGTAT	200
40	CAAGGTTGTC	GACCTGTTGG	CTCCTTACGC	TCGTGGTGGA	AAGATTGGTC	250
	TCTTCGGAGG	TGCTGGTGTC	GGAAAGACTG	TCTTCATTCA	GGAGCTGATT	300
	GTAAGGAGAC	ACACTGTCTA	CTGGCTGAGC	ATTAGCTAAC	GGCAGGCAGA	350
	ACAACATCGC	CAAGGCCAC	GGTGGTTTCT	CTGTCTTCAC	TGGTGTTCGGT	400
	GAGCGTACCC	GTGAGGGTAA	CGATCTGTAC	CACGAGATGC	AGGAGACTTC	450
45	CGTCATTGAG	CTTGACGGTG	ACTCCAAGGT	CGCCCTCGTC	TTCCGGTCAGA	500
	TGAACGAGCC	CCCGGGTGCC	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACT	550
	GTTGCTGAGT	AAGTCTTGAA	TTCATCTGTG	TGACAACGTC	GTGGCTAATG	600
	GGAAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGTA	GAACTGCCTG	TGAGACATAC	ACTGACTTCG	700
50	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTTCCGAGG	TGTCCGCTCT	750
	TCTTGGTTCG	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACC	CTCGCCATTG	800
	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGGTTCATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTGTA	CTGACCCTGC	900
	CCCCGCCACC	ACCTTCGCCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
55	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCCG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
	CACCCGCGTT	CAGCAGATTC	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTGCG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTGCG	1200
60	CCAGGTCTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250

TCCGATCATT	CAAGGCTATC	TTGACTGGTG	AGGGTGACGA	CCTTCCCGAG	1300
GGTGAGTCTC	GACTATCTCC	GCATTCATAG	CGTATAACTG	ACA	1343

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2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
- (B) STRAIN: ATCC 26947

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

TTCAGGAGTT	GATTGTATGT	TCACCTGCAA	CATAAGACTT	CCCATTCTCC	50
ACTCTTTTCT	AACTCTTCAC	AGAACAACAT	TGCCAAGGCT	CACGGTGGTT	100
ACTCTGTCTT	CACTGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGATCTG	150
25 TACCACGAAA	TGCAGGAGAC	TGGTGTCATT	CAGCTCGAGG	GTGAATCTAA	200
GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCCAGGT	GCCCCGTGCCC	250
GTGTGCGCCT	TACCGGTCTG	ACCATCGCCG	AGTACTTCCG	TGACGAGGAA	300
GGTCAGGATG	TGCTGCTCTT	CATTGACAAC	ATTTTCCGTT	TCACCCAGGC	350
CGGTTCTGAG	GTGTCTGCCC	TTCTTGGTCG	TATCCCCTCC	GCTGTGCGTT	400
30 ACCAGCCCAC	TCTGGCCGTC	GACATGGGTG	GTATGCAGGA	GCGTATTACC	450
ACCACCACCA	AGGGTTCCAT	TACCTCCGTC			480

35 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1174 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
- (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

50

CTCGAACAAG	AYAACTTGCC	YGCCATTTTG	AACGCCCTTG	AAGTCAAGGA	50
YCACTCTGGT	GGACGTCTCG	TYCTCGAAGT	CTCTCAACAT	TTGGGTGAGA	100
ACACTGTCCG	TACTATTGCT	ATGGATGGTA	CTGAAGGTAA	GTTATGTYCA	150
TCCCANNGGA	TACAGTCARA	CAGMAATGTC	TAGTGGTTAT	AGCAGYAGCA	200
55 GATGATTGAC	CAATATGTTA	GGTCTTGTCC	GGTGGTCAAA	AGGTTGTTGA	250
CACTGGTGCT	CCCATTACCA	TCCCCGTTGG	TAAGGAAGTC	CTTGGTCGTA	300
TCATCAACGT	TATTGGTGAA	CCCATTGATG	AACGTGGTCC	CATTGACGCC	350
AAGACTCACC	GTCCTATTCA	CGCTGAAGCT	CCCGAATTCC	TTGATCAATC	400
CCCCACTCCC	GAAATCCTCG	AGACTGGTAT	CAAGGTYGTC	GATTTGTTGG	450
60 CTCCTTATGC	TCGTGGTGGT	AAGATTGGTC	TCTTCGGTGG	TGCTGGTGTC	500

	GGTAAGACTG	TCTTGATTCA	AGAATTGATT	AACAACATYG	CCAAGGCTCA	550
	CGGTGGTTAC	TCTATCTTCT	GTGGTGTCCG	TGAACGTACT	CGTGAGGGTA	600
	ACGATTTGTA	CCATGAAATG	ATTGAAACCG	GTGTCATTCA	ATTGGAAGGC	650
	GAGTCCAAGT	GTGCTCTCGT	CTTTGGTCAA	ATGAACGAAC	CCCCAGGTGC	700
5	TCGTGCCCCG	GTCGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCCGTG	750
	ATGATGAGGG	TCAAGATGTC	TTGCTTTTCA	TTGATAACAT	TTTCAGATTC	800
	ACTCAAGCTG	GTTCTGAGGT	ATCTGCCCTT	TTGGGTTCGTA	TTCTTCCGC	850
	TGTCGGTTAC	CAACCCACTC	TTTCCACYGA	TATGGGTGGT	ATGCAAGAGC	900
	GTATTACTAC	CACCAAGAAC	GGTTCCATTA	CCTCCGTCCA	AGCTGTCTAC	950
10	GTCCCTGCTG	ATGATTTGAC	CGATCCTGCT	CCTGCCACCA	CTTTTGCTCA	1000
	CTTGGATGCC	ACCACTGTCT	TGTCTCGTTC	CATCGCTGAA	TTGGGTATCT	1050
	AYCCCGCTGT	CGATCCTCTT	GATTCCAAGT	CTCGTATCCT	CGATCCCCGT	1100
	ATTGTCGGTG	ATGAGCACTA	CAAGGTTGCC	ACTGAAGTTC	AACAAATCCT	1150
	CCAAACTAC	AAGTCTCTCC	AAGA			1174

2) INFORMATION FOR SEQ ID NO: 772

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
- (B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

	AGGAGCTTAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
35	ACTGGTGTCG	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	100
	GCAAGAGACT	TCCGTCATTG	AGCTTGACSG	CGAGTCCAAG	GTCGCTCTCG	150
	TGTTTCGGTCA	GATGAACGAG	CCCCCGGGTG	CCCGTGCCCG	TGTTGCCCTG	200
	ACTGGTCTTA	CCATCGCTGA	GTACTTCCGT	GATGCCGAGG	GTCAGGATGG	250
	TAAGTTCTAT	AACTCTTGTC	GCAAAGGTTT	CATTCTGGTC	GCTAACTTGC	300
40	TCAGTGCTCC	TGTTTCATCGA	CAACATTTTC	CGTTTCACCC	AGGCTGGTAT	350
	GGAGGTGTCT	GCCCTCCTCG	GTCGTATTCC	TTCTGCCGTC	GGTTACCAAC	400
	CTACTCTCGC	CGTCGACATG	GGTGGTATGC	AAGAGCGTAT	TACCACTACC	450
	AAGAAGGGAT	CCATTAC				467

2) INFORMATION FOR SEQ ID NO: 773

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
- (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

```

5   TTGCCAAGGC CCACGGTGGT TACTCTGTCT TCACTGGTGT CGGTGAGCGT      50
    ACCCGTGAGG GTAACGATCT GTACCACGAA ATGCAGGAAA CCTCCGTCAT      100
    TCAGCTTGAT GGCAGAGTCCA AGGTCGCGCT TGTCTTCGGT CAGATGAACG      150
    AGCCCCCTGG TGCCCGTGCT CGTGTGCTC TTACTGGTCT TACCGTTGCC      200
    GAGTACTTCC GTGATGAGGA GGGTCAGGAT GGTAAGTTAT ATCGTTTTTA      250
    TTATCTTCTT TGCCACCACC CCTCTACGAA TCCATGCCTC CGTTGGTGAA      300
    GGCATCGTTT GTAGGGCGGG TCGGAGTTTG CGGCAATTTC TGCCGTCGGC      350
10  TTGAAGCCGC GGATGCCCCGA TGTGTGACGC GTATCGATGC TAACAACAAT      400
    GACAACAGTG CTTCTCTTCA TTGACAACAT TTTCCGATTC ACCCAGGCCG      450
    GTTCCGAGGT GTCTGCCCTT CTCGGTCGTA TTCCCTCTGC CGTCGGTTAC      500
    CAGCCCCTC TTGCCGTAGA CATGGGTGCC ATGCAGGAAC GTATTACCAC      550
    CACCAAGAAG GGTTCGATTA CCTCCGTC      578
15

```

2) INFORMATION FOR SEQ ID NO: 774

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20  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1123 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25
    (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Rhizopus oryzae
30  (B) STRAIN: ATCC 56015

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

```

35  AACTTACCYG CTATCTTGAA CGCTCTCGAA GTCCAAGATC ACTCTGGTGG      50
    ACGTCTTGTC CTTGAAGTTC GCTCAACACT TGGGTGAAAA TACTGTCCGT      100
    ACTATTGCTA TGGATGGTAC TGAAGGTAAG CTATACTATA ACCGKTAT      150
    CCGAGTATGA TATTAAGTTG AAAAAAGGTC TCGTYCGTGG TCAAAAGGTT      200
    ATTGACACTG GTGCTCCCAT TACCATTCTT GYTGGTAAGG AAGTTCTCGG      250
    TCGTATCATT AACGTCATTG GTGAACCCAT CGATGAACGT GGTCCTATCA      300
40  ACGCCAAGAG CCAACGTCCC ATTCACGCCG AAGCTCCCGA ATTCGTTGAC      350
    CAATCTCCTA CTCCCGAAAT TCTTGAAACT GGTATCAAGG TTGTCGACTT      400
    GTTGGCTCCT TATGCTCGTG GTGGTAAGAT TGGTCTTTTC GGTGGTGCTG      450
    GTGTCGGTAA GACTGTGTTG ATTCAAGAAT TGATTAACAA CATCGCCAAG      500
    GCTCACGGTG GTTACTCTAT TTTCTGTGGT GTCGGTGAAC GTACTCGTGA      550
45  AGGTAACGAT CTTTACCACG AAATGATTGA AACTGGTGTC ATCAAGCTCG      600
    ATGGTGACTC CAAGTGTGCT CTTGTCTTTG GTCAAATGAA CGAACCCCCA      650
    GGAGCTCGTG CCCGTGTTGC CTTGACTGGT TTGACCATTG CTGAATACTT      700
    CCGTGATGAT GAAGGTCAAG ATGTGTTGCT TTTCATTGAT AACATTTTCC      750
    GTTTCACCCA AGCTGGTTCW GAAGTATCTG CCCTTTTGGG TCGTATTCCC      800
50  TCCGCTGTCG GTTACCAACC CACTCTTTCT ACTGATATGG GTGGTATGCA      850
    AGAACGTATT ACAACCACCA AGAACGGTTC CATTACATCC GTCCAAGCTG      900
    TCTACGTCCC TGCTGATGAT TTGACCGATC CTGCTCCCGC CACCACTTTT      950
    GCTCACTTGG ATGCCACCAC TGTCTTGTCT CGTTCCATTG CCGAATTGGG      1000
    TATTTACCCT GCCGTCGATC CTCTTGAYTC CAAGTCTCGT ATCTTGGATC      1050
55  CTCGTATCGT TGGTGACGAA CACTACAAGG TCGCTACCGA AGTTCAACAA      1100
    ATCCTTCAAA ACTACAAGTC TCT      1123

```

60 2) INFORMATION FOR SEQ ID NO: 775

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Scopulariopsis koningii*
 (B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

```

15  ATTCAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT      50
    GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG      100
    AAATGCAGGA GACTTCGGTC ATTCAGCTCG AGGGCGAGTC CAAGGTCGCG      150
    CTTGTGTTTC GTCAGATGAA CGAGCCCCC GGTGCCCGTG CCCGTGTTCG      200
20  CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG      250
    ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG      300
    ACAACTAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG      350
    GTTCCGAGGT GTCCGCGCTT CTCGGCCGTA TCCCTCTGCG CGTCGGTTAC      400
    CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC      450
25  GACTCAGAAG GGCTCGATTA CCTCGGT      477
  
```

2) INFORMATION FOR SEQ ID NO: 776

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

```

45  TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AAACAGAAGC      50
    TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT      100
    TCGAGTATTA ATTGTTTTTA TAGAACAAAC TTGCCAAGGC TCACGGTGGT      150
    TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT      200
    CTACCATGAA ATGCAGGAGA CCCGTGTCAT TCAGCTTGAT GGCGAGTCCA      250
50  AGGTCGCCCT GGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCGTGCC      300
    CGTGTTGCTC TTA CTGTTT GACCATTGCT GAGTACTTCC GTGATGAGGA      350
    AGGTCAAGAC GGTGAGTTTY TTATGGATAA AARATTTTTT TTTTTTTTTT      400
    TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT      450
    CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCCGAA GTGTCTGCCC      500
55  TGCTTGGTCG TATCCCATCT GCCGTCGGTT ACCAACCAC TCTTGCCGTC      550
    GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT      600
    TACCTCCGTC      610
  
```

2) INFORMATION FOR SEQ ID NO: 777

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

GGAGTTGATT	GTAAGTCATT	TGAAACCCAG	CCCCAAGAAA	CAGAAGCTAG	50
GTGAAAATTG	GACAATTGAA	CAATTTAGCC	CTTGGAGAAA	AGAAATTTTCG	100
AGTATTAATT	ATTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
20 TCTGTCTTCA	CTGGTGTCGG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCCGT	300
GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
TCAAGACGGT	GAGTTTCTTA	TGGATGAAAG	ATTTTTTTTT	TTCAAGAAAT	400
25 TCATGTTCTA	ACAAAGTGTA	TTCTAGTGCT	TCTCTTCATC	GACAACATTT	450
TCCGTTTCAC	TCAGGCTGGT	TCCGAAGTGT	CTGCCCTGCT	TGGTCGTATC	500
CCATCTGCCG	TCGGTTACCA	ACCCACTCTT	GCCGTCGACA	TGGGTGGTAT	550
GCAGGAACGT	ATTACCACCA	CCAAGAAGGG	ATCCATTACC	TCC	593

2) INFORMATION FOR SEQ ID NO: 778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

CCGTGGTCAA	GAAGTTATTG	ACACTGGTGC	CCCAATTACC	ATTCCTGTTG	50
GTCGTGGTAC	TCTTGGTAGA	ATTATCAACG	TCATTGGTGA	ACCAATTGAC	100
50 GAACGTGGCC	CTATCAAGGC	TTCTAAGTAT	GCTCCTATCC	ATACTGAACC	150
ACCAACCTTT	GCTGAACAAT	CTACTTCTGC	TGAAGTTCTT	GAAACCGGTA	200
TCAAGGTTGT	CGATCTTCTT	GCTCCTTACG	CCCGTGGTGG	TAAGATTGGT	250
CTTTTCGGTG	GTGCTGGTGT	CGGTAAGACT	GTCTTCATTC	AAGAACTTAT	300
TAACAACATT	GCCAAGGCTC	ACGGTGGTTT	CTCTGTCTTC	ACTGGTGTCG	350
55 GTGAAAGAAC	CCGTGAAGGT	AACGATCTTT	ACCGTGAAAT	GAAGGAAACT	400
GGTGTCATCA	ACCTCGAAGG	TGACTCCAAG	GTGCTCTCTG	TTTTCGGTCA	450
AATGAACGAA	CCTCCAGGTG	CCCGTGCCCG	TGTCGCTTTG	ACTGGTCTTA	500
CCATTGCCGA	ATACTTCCGT	GATGAAGAAG	GACAAGATGT	CTTGCTTTTC	550
GTTGACAACA	TTTTCAGATT	CACCCAAGCC	GGTTCTGAAG	TCTCTGCTCT	600
60 TTTGGGTTCG	ATTCCATCTG	CCGTCGGTTA	CCAACCTACC	CTTGCTACCG	650

	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCCGTC	700
	ACATCTGTCC	AAGCCGTCTA	TGTCCCAGCA	GACGATTTGA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
5	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTC	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
10	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 22864

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

30	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTCGAGAC	TCCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTA CTGGTGA	GTTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
35	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACCTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTCT	TGCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
40	CTATCGACTC	CATCGACCTT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCGT	600
	CGGTCTGTGT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
45	CGTCTCCGTG	AAGGAGGTTT	GTCGTGGAAA	CGTTGCTGGT	GACTCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCAGGT	CATCGTCCTC	850
	AACCACCCTG	GTCAGGTCCG	TGCTGCTTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
50	GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTCACCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

55 2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

10 TACTTGTAAG TGGTCTCAAG ATCGTTACAA CGAAATTGTT AAGGAAGTTT 50
 CTTCTTTCAT CAAGAAGATT GGTTACAATC CTAAATCCGT TCCTTTCGTY 100
 CCTATCTCTG GTTGGCACGG TGATAACATG TTGGAAGCTT CTACCAACAT 150
 GCCTTGGTAC AAGGGATGGA CCAAGGAAAC TAAAGCTGGT TCTTCCACTG 200
 15 GTAAGACTCT CTTAGAAGCC ATTGACAGCA TTGAACCTCC TACCCGTCCT 250
 TCTGACAAGC CTTTACGTCT TCCTTTACAA GATGTTTACA AGATTGGTGG 300
 TATTGGTACT GTCCCTGTTG GTCGTGTTGA AACTGGTGTC ATCAAGGCTG 350
 GTATGGTTGT TACYTTCGCT CCCGCTAACG TCACCACTGA AGTTAAGTCC 400
 GTTGAAATGC ATCACGAACA ATTAGAACAA GGTGTTCCCTG GTGACAACGT 450
 20 TGGTTTCAAC GTCAAGAACG TTTCCGTTAA GGATATCCGT CGTGGTAACG 500
 TCTGTTCCGA CTCCAAGAAC GACCCCGCTA AGGAATCTGC TTCCTTCAAC 550
 GCTCAAGTTA TCGTCTTGAA CCACCCTGGT CAAATTGGTG CTGGTTATGC 600
 CCCAGTTCTT GACTGTCACA CTGCTCACAT TGCTTGTAAG TTCGCTGAAT 650
 TATTAGAAAA GATCGATCGT CGTTCGCGTA AGAACTCGA AGATGCTCCT 700
 25 AAATTCGTTA AATCTGGTGA CTCTGCTATC GTTAAGATGG TTCCTTCCAA 750
 GC 752

30 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

45 CAAGTGGTCT GAGGACCGTT ACCAGGAAAT CATCAAGGAG ACCTCCAAC 50
 TCATCAAGAA GGTCGGCTAC AACCCCAAGC ACGTTCCCTT CGTCCCCATC 100
 TCCGGTTTCA ACGGAGACAA CATGATTGAG GCCTCCACCA ACTGCCCTG 150
 GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC 200
 50 TCCTTGAGGC CATCGACGCC ATCGACCCTC CTGTCCGTCC TACCGACAAG 250
 CCCCTCCGCC TTCCCTCCA GGATGTTTAC AAGATTGGTG GTATTGGCAC 300
 GGTCCCGTCC GGTCGTGTCG AGACCGGTAT CATCAAGCCC GGTATGGTCG 350
 TCACCTTCGC CCCCCTGGT GTCACCACCG AAGTCAAGTC CGTCGAGATG 400
 CACCACGAGC AGCTTACTGA GGGTGTCCCC GGTGACAACG TCGGCTTCAA 450
 55 CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGGTAAC GTTGCCGGTG 500
 ACTCCAAGAA CGACCCCCC AAGGGTTGCG AGTCCTTCAA CGCCAGGTC 550
 ATCGTCCTCA ACCACCCTGG TCAGGTCGGT GCCGGTTACG CCCAGTCCT 600
 TGAATGCCAC ACTGCCACCA TTGCCTGCAA GTTCTCCGAG CTCCTCGAGA 650
 AGATCGACCG CCGTACCGGA AAGTCTGTTG AGAACTCCCC CAAGTTCATC 700
 60 AAGTCCGGTG ACGCCGCCAT CGTCAAGA 728

2) INFORMATION FOR SEQ ID NO: 782

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

20	TGAAGTCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACTC	CCAAGTAAGG	CTCAACAGAC	ACAACAAGCA	AATGCATACT	100
	CGCTAACCTA	TTCACCCACC	ACAGGTACAA	CGTCACCGTC	ATTGACGCCC	150
	CCGGTCACCG	TGATTTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGCGCCA	TTCTCATCAT	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCCGG	250
25	TATCTCCAAG	GACGGTCAGA	CCCGTGAGCA	CGCTCTTCTC	GCCTACACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	350
	TGGTCTGAGG	CCCGTTACCA	GGAGATCATC	AAGGAGACCT	CCGGTTTCAT	400
	CAAGAAGGTC	GGCTTCAACC	CCAAGCACGT	TCCCTTCGTG	CCCATCTCCG	450
	GTTTCAACGG	TGACAACATG	ATCGACGTCT	CCACCAACTG	CCCCTGGTAC	500
30	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGCCATCG	ACCCCCCAC	TCGTCCCACC	GACAAGCCCC	600
	TCCGTCTTCC	CCTYCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGCACGGTT	650
	CCCGTCGGTC	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTCAC	700
	CTTCGCCCCC	GCTGGTGTCA	CCACTGAGGT	CAAGTCCGTC	GAGATGCACC	750
35	ACGAGCAGCT	TCCCGAGGGT	CTCCCCGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGCAACGTCG	CCGGTGACTC	850
	CAAGAACGAC	CCCCCAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTCGGCGCCG	GCTACGCGCC	CGTCCTCGAC	950
	TGCCACACTG	CTCACATTGC	TTGCAAGTTC	TCTGAGCTCC	TCGAGAAGAT	1000
40	CGACCGCCGT	ACCGGCAAGT	CCATTGAGGC	CAGCCCCAAG	TTCATCAAGT	1050
	CTGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	TATGTGCGTT	1100
	GAGGCCTTCA	CCGACTACCC	CCCTCTTGA	CGTTTCGCCG	TCCGT	1145

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

	GCTCAAGGCT	GAGCGTGAGC	GTGGTATCAC	CATTGACATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	ATGGTCACCG	TCATCGGTAT	GCTTTATCTG	100
	TTTCCCATT	ATAGTTGCGA	CAAGTAACTA	ATAAAAAGTA	GATGCCCCCG	150
5	GACACCGTGA	CTTCATCAAG	AACATGATTA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATTC	TCATCATTCG	TGCCGGTACT	GGTGAGTTTC	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCT	TTCACCCTCG	300
	GTGTCAAGCA	GCTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAACTGG	350
	TCTGAGTCCC	GTTTCGGTGA	AATCATCAAG	GAAGTCACCA	ACTTCATCAA	400
10	GAAGGTCGGC	TACGACCCCA	AGGGTGTCCC	ATTCGTCCCA	ATCTCTGGCT	450
	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAACTGCCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CATCTGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCCTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
15	GTACCAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	750
	ACCACCAGCA	GCTCGTTCAG	GGTGTTCCTG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAACG	TCTCTGTCAA	GGAAGTCCGC	CGTGGTAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAG	GCCCAGGTCA	900
20	TCGTCCTCAA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCGA	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TCACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
25	C					1151

2) INFORMATION FOR SEQ ID NO: 784

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
 (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

45	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GACTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCCTTCTGA	250
50	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
	GTTGTCAACT	TCGCTCCCGC	TGCTGTCAAC	ACTGAAGTTA	AGTCCGTGTA	400
	AATGCATCAC	GAAACCCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
55	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAATTCATT	650
	GAGAAGATTG	ATCGTCGTTC	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
60	CTATAATGAT	GATTGCTCCT	TCAATTTTTG	ACATAATTTG	ATGATCTGAA	800

TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTA G GT	850
AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTCGTCAAG	TCTGGTGACT	950
CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

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2) INFORMATION FOR SEQ ID NO: 785

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phialaphora verrucosa*
 (B) STRAIN: ATCC 38561

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
25 TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCT	100
GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
30 GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCC	CCTGGTACAA	450
GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
TCGAGGCCAT	CGACGCGATT	GACCCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
35 CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
GCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCG	GCTTCAACGT	750
CAAGAACGTC	TCCGTCAAGG	AGGTTTCGTCG	TGGAAACGTT	GCCGGTGACT	800
40 CCAAGAATGA	CCCCCCCAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
GTCCTCAACC	ACCCTGGTCA	GGTCCGTGCC	GGCTACGCCC	CGGTCTTGGA	900
TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
45 TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saksenaea vasiformis*

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448

(B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

5	ACCACCAAGT	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	50
	CGGYTTCATC	AAGAAGGTCG	GCTTCAACCC	CAAGCACGTT	CCCTTCGTGC	100
	CCATCTCCGG	TTTCAACGGT	GACAACATGA	TCGACGTCTC	CACCAACTGC	150
	CCCTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACCGGCAA	200
	GACCMTCCTC	GAGGCCATTG	ACGCCATCGA	CCCCCYAGY	CGTCCCACCG	250
10	ACAAGCCCCCT	YCGTCTTCCC	CTMCAGGATG	TYTACAAGAT	TGGCGGTATT	300
	GGCACGGTTC	CCGTCGGTTCG	TGTYGAGACC	GGTRCCATCA	AGGGTGGCAT	350
	GGTCGTACAC	TTCCCCCCCCG	CTGGTGTAC	CACTGAGGTC	AAGTCCGTCG	400
	AGATGCACCA	CGAGCAGCTC	GCCGAGGGTS	TCCCCGGTGA	CAACGTCGGC	450
	TTCAACGTCA	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GCAACGTTGC	500
15	CGGTGACTCC	AAGAACGACC	CCCCCAAGGG	CTGCGACAGC	TTCAACGCCC	550
	AGGTCACTCGT	CCTCAACCAC	CCCGGTCAGG	TCGGCGCCGG	CTACGCGCCS	600
	GTCCTSGACT	GCCACACTGC	TCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	650
	CGAGAAGATC	GACCGCCGTT	CCGGCAAGTC	CATCGAGTCC	GGCCCCAAGT	700
	TCATCAAGTC	TGGTGACGCC	GCCATCGTCA	AGATGGTTCC	CTCCAAGCCC	750
20						

2) INFORMATION FOR SEQ ID NO: 787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
 (B) STRAIN: ATCC 32330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

40	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCTCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CACGTCACCG	TCATTGATGC	CCCCGGCCAT	100
	CGTGATTTC	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CTGACTGCGG	150
	TATCCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTTCGAGGCT	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TTGCCCTTAC	CCTCGGTGTC	250
	CGTCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACTCGACCA	AGTACTCTGA	300
45	GGCCCGTTAC	AACGAAATCG	TCAAGGAGGT	CTCCACCTTC	ATCAAGAAGA	350
	TCGGTTTCAA	CCCCAAGTCC	GTTCCCTTCG	TCCCCATCTC	TGGCTGGAAC	400
	GGTGACAACA	TGTTGGAGGA	GTCCTCCAAC	ATGCCCTGGT	TCAAGGGCTG	450
	GAAGAAGGAG	ACCAAGGCTG	GCGAGAAGTC	CGGCAAGACC	CTCCTTGAGG	500
	CCATTGACAA	CATTGACCCC	CCGGTCCGTC	CCTCGGACAA	GCCCCCTCGT	550
50	CTTCCCCCTC	AGGATGTCTA	CAAGATCGGT	GGTATCGGCA	CAGTCCCCGT	600
	CGGTTCGTGTC	GAGACTGGTG	TCATCAAGGC	TGGTATGGTC	GTGACCTTCG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
	CAGCTCGTCG	AGGGTGTCCC	CGGTGACAAC	GTCGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTC	AAGGATATCC	GCCGTGGTAA	CGTCTGCTCT	GACTCCAAGA	800
55	ACGACCCCGC	CAAGGAGTCT	GCCTCGTTCA	CCGCCCAGGT	CATCGTCCTG	850
	AACCACCCCG	GTCAGATCGG	TGCCGGTTAC	GCCCCGGTTC	TTGACTGCCA	900
	CACCGCTCAC	ATTGCCTGCA	AGTTCGCTGA	GCTCCTCGAG	AAGATCGACC	950
	GTCGTTCCGG	YAAGAAGCTC	GAAGAGTCCC	CCAAGTTCGT	CAAGTCGGGT	1000
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1050
60	CTACACTGAG	TACCCCCCTC	TTGGCCGTTT	CGCC		1084

2) INFORMATION FOR SEQ ID NO: 788

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

20	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AATGTCACCG	TCATTGGTAT	GTTTTTCCTT	100
	ACCTTTCCCC	TCCATCGTCT	TGCTGTGCCA	TAACTAACGA	GAGTAGACGC	150
	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	200
	CTGACTGTGC	TATTCTCATC	ATTGCTGCCG	GTACTGGTGA	GTTTCGAGGCT	250
25	GGTATCTCCA	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TCGCCCTTCAC	300
	CCTTGGTGTC	AAGCAGCTCA	TCGTTGCCAT	CAACAAGATG	GACACCACCA	350
	ACTGGTCCGA	GGACCGTTTC	AAGGAAATCA	TCAAGGAAGT	CACCAACTTC	400
	ATCAAGAAGG	TTGGCTACGA	CCCCAAGGGT	GTTCCATTCT	TTCCAATCTC	450
	TGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCAGCAAC	TGCCCATGGT	500
30	ACAAGGGATG	GAACAAGGAG	ACCAAGGCCG	GTGGTGCCAA	GACTGGCAAG	550
	ACCCTYCTCG	AGGCCATCGA	TGCCATCGAC	ATGCCAACCC	GTCCTACCGA	600
	CAAGCCCCTY	CGTCTCCAC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	650
	GAAGTGTACC	AGTCGGTCGT	GTTGAGACCG	GTATCATCAA	GCCTGGTATG	700
	GTCGTCACCT	TCGCCCCCTG	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	750
35	AATGCACCAC	CAGCAGCTTC	AGCAGGGTGT	CCCCGGTGAC	AACGTCGGCT	800
	TCAACGTCAA	GAACGTTTCC	GTCAAGGAAG	TCCGCCGTGG	TAACGTTGCC	850
	GGTGACTCCA	AGAACGACCC	ACCATCCGGC	TGTGCCTCCT	TCAACGCCCA	900
	GGTCATCGTC	CTCAACCACC	CCGGCCAGAT	CGGTGCTGGT	TACGCCCCAG	950
	TCCTCGACTG	CCACACTGCT	CACATTGCTT	GCAAGTTCGC	TGAGCTCCTC	1000
40	GAGAAGATTG	ACCGCCGTAC	CGGTAAATCC	GTCGAAGCCA	ACCCCAAGTT	1050
	CGTCAAGTCT	GGTGATGCCG	CTATCGCCAA	GATGGTTCCC	TCCAAGCCCA	1100
	TGTGCGTTGA	GGCTTTCACT	GACTACCCCC	CACTTGGTCG	TTTCGCCGTC	1150
	CGTGA					1155

2) INFORMATION FOR SEQ ID NO: 789

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

	TCAAGGCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACCC	CCAAGTACAA	TGTCACCGTC	ATTGGTATGT	TTCTCTTTAC	100
5	CTTTCCCCTC	CATCGTCTTG	CTGTGCCATA	ACTAACGAGA	GTAGACGCCC	150
	CCGGTCACCG	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGTGCTA	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	250
	TATCTCCAAG	GATGGCCAGA	CCCGTGAGCA	CGCTCTGCTC	GCCTTCACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	350
10	TGGTCCGAGG	ACCGTTTCAA	GGAAATCATC	AAGGAAGTCA	CCAACTTCAT	400
	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTCGTT	CCAATCTCTG	450
	GTTTCAACGG	TGACAAACATG	ATTGAGGCCT	CCACCAACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
15	AGCCCCTCCG	TCTCCCACCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCTGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCACCA	GCAGCTTCAG	CAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	850
20	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCCTCCTTC	AACGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAC	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGTTTCCATC	CAAGCCTATG	1100
25	TGCGTTGAGG	CTTTCACCTGA	CTACCCCCCA	CTTGGTTCG		1138

2) INFORMATION FOR SEQ ID NO: 790

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

45	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCTTACC	250
50	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCAGTA	350
	TGGTCGTCAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
55	CCGGTGACTC	CAAGAACGAC	CCCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
60	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

2) INFORMATION FOR SEQ ID NO: 791

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Aspergillus fumigatus*
 15 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

	CGCTATTGTC	GTTGTTGCTG	CCTCCGACGG	TCAGATGTAG	GTGGAACATC	50
20	TTGGGAAATA	CGTCGTAAAA	CACGGCGCTT	ACGTTTTTCG	GAATAGGCC	100
	CAGACTCGTG	AGCATTGCT	GCTCGCCCGC	CAGGTTGGTG	TCCAGAAGAT	150
	CGTTGTCTTC	GTCAACAAAA	TCGATGCTAT	TGATGATCCG	GAGATGCTGG	200
	AACGGGTCGA	ACTCGAGATG	CGTGAGCTGC	TGAACAGCTA	CGGTTTCGAG	250
	GGTGAAGAGA	CTCCGATCAT	TTTCGGTTCC	GCTCTCTGTG	CTCTCGAAGG	300
25	ACGCCGTGAC	GACATCGGTA	AAGACAGAAT	TGAGCAGCTT	ATGAACGCTG	350
	TCGACACCTG	GATCCCCACT	CCTCAGCGTG	ACCTCGACAA	ACCTTCTTGT	400
	ATGTCTGTCTG	AGGAAGTGTT	CTCTATCGCC	GGCCGTGGTA	CCGTGGCTTC	450
	TGGTCGTGTC	GAGCGTGGTA	TCTTGAAGAA	GGACTCTGAG	GTTGAGATTG	500
	TTGGAGGCTC	CTTCGAACCC	AAGAAGACCA	AAGTCACCGA	CATTGAAACC	550
30	TTCAAGAAGA	GCTGTGATGA	ATCGCGTGCT	GGTGACAAC	CTGGTCTCCT	600
	CCTGCGTGGT	ATCCGACGTG	AAGACGTCAA	GCGTGGTATG	GTCATTGCTG	650
	TTCCCGGCAG	CACCAAAGCT	CACGACAAGT	TCCTCGTCTC	CATGTACGTC	700
	CTGACCGAGG	CGGAGGGTGG	TCGTCGTACT	GGCTTCGGTG	CCAACTACCG	750
	TCCCCAAGTC	TTCATCCGTA	CTGCAGGTAA	GTTCCCGCAC	ACCGTGTCCA	800
35	GATCTTCCGA	GAGATTAGCG	ATATATGCTA	ATGATTCATC	AGACGAGGCT	850
	GCTGACCTCA	GCTTCCCTGA	CGGCGACCAA	TCTCGCAGAG	TTATGCCTGG	900
	TGACAACGTC	GAGATGATCC	TGAAGACCCA	CCACCCTGTT	GCTGCTGAGG	950
	CTGGTCAA					958

40

2) INFORMATION FOR SEQ ID NO: 792

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

	CGTTGTGCGCA	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACG	50
	GATGAAAGGA	TTTGACGTTT	CTAACATCAT	TCTAGGCCTC	AGACCAGAGA	100
60	ACATTTGCTC	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	150

	TTAACAAGGT	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	200
	CTTGAAATGC	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	250
	CCCCATCATT	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	300
	AGCTTGGTGT	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	350
5	ATCCCCACCC	CCGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	400
	GGAAGTGTTT	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	450
	AGCGTGGTAT	CCTCAAGAAG	GATTCCGACG	TCGAAATTGT	TGGTGGCTCT	500
	ACCACCCCTA	TCAAGACCAA	GGTCACAGAT	ATCGAAACCT	TCAAGAAGTC	550
	CTGCGATGAA	TCTCGAGCTG	GTGACAACTC	TGGTCTCCTT	CTCCGAGGTA	600
10	TCAAGCGTGA	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	650
	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTGCTA	ACTTGTATTT	CCTTCCGTAG	ATCGAAGCCG	ATCTTTCAGC	850
15	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTTG	TGCCGA		936

20 2) INFORMATION FOR SEQ ID NO: 793

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

35 2) INFORMATION FOR SEQ ID NO: 794

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

50

GACGACAAGT CGGTGAACTT

20

55 2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

453

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

10 ACTTGACACGC GATGTGGCAG

20

2) INFORMATION FOR SEQ ID NO: 796

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

25

GGTCCAATGC CWCAAACWAG A

21

30 2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT

27

45

2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

60

TGGTTGTCCC AGCCGATCGT TT

22

5 2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

20 ACCTGTGAAT ACAAGCAATC T

21

25 2) INFORMATION FOR SEQ ID NO: 800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

40 GATGAAATCT TCAACGAAGT TGAT

24

2) INFORMATION FOR SEQ ID NO: 801

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

60 ACAACACCGA GAAGATCCCA

20

2) INFORMATION FOR SEQ ID NO: 802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

TTGCCATTTT TGGTTTCGTT

2) INFORMATION FOR SEQ ID NO: 803

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

ACTTCAGTGG TAACACCAGC

2) INFORMATION FOR SEQ ID NO: 804

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

CCTGGGACGG CCTCTGGCAT

2) INFORMATION FOR SEQ ID NO: 805

(i) SEQUENCE CHARACTERISTICS:

456

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTTCCA TCTTAGCAGT

20

15

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

35

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

AAAGTGGCTT CAAAGGTTGC

20

55 2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

457

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

10

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

25

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

40

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

55

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

GTIACIGGIT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 813

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

25 AATCYGTYGA AATGCAYCAC GA

22

2) INFORMATION FOR SEQ ID NO: 814

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814

40

GCIGGCACGT ACACIGCCTG

20

45 2) INFORMATION FOR SEQ ID NO: 815

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815

55

TGGTGATYT CKACRGACTT

20

60

2) INFORMATION FOR SEQ ID NO: 816

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

2) INFORMATION FOR SEQ ID NO: 818

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

AGCCGGGCTG GATCTTCTTC

2) INFORMATION FOR SEQ ID NO: 819

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

TCGAGCTTCT GGAGGAAGAG

20

5 2) INFORMATION FOR SEQ ID NO: 820

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

20 GAAGGAGGTG TCTGCTTACA C

21

25 2) INFORMATION FOR SEQ ID NO: 821

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

40 GGCGCAAACG TCACCACATC A

21

2) INFORMATION FOR SEQ ID NO: 822

45 (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Trypanosoma brucei*

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

60 CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

GAGCGGTATG AYGAGATTGT

20

2) INFORMATION FOR SEQ ID NO: 824

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

GGCTTCTGCG GCACCATGCG

20

2) INFORMATION FOR SEQ ID NO: 825

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

ATGAGCARCG SAACCATCGT TCAGTG

26

2) INFORMATION FOR SEQ ID NO: 826

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

462

TCGATCGTGC CGACCATGTA GAACGC

26

5

2) INFORMATION FOR SEQ ID NO: 827

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 446 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
- (B) STRAIN: ATCC 19402

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

	CACCAACTTG	CTAAATGGGG	AGATGCCCAG	ATTGTTGTAT	ATATAGGCTG	50
	TGGAGAACGT	GGAAATGAAA	TGACAGATGT	TCTTAATGAG	TTTCCAGAAC	100
	TTAAAGATCC	TAAGACTGGC	AAATCAATAA	TGGAAAGAAC	AGTTTTAATA	150
25	GCAAATACTT	CTAATATGCC	AGTTGCAGCC	CGTGAAGCTT	GTATATATAC	200
	AGGAATCACA	ATAGCAGAAT	ATTTTAGAGA	TATGGGATAT	TCAGTAGCAC	250
	TTATGGCGGA	TTCCACTTCA	CGTTGGGCAG	AGGCATTAAG	AGAAATGTCT	300
	GGAAGACTTG	AAGAAATGCC	TGGTGATGAA	GGTTACCCAG	CTTATTTAGG	350
	ATCAAGACTT	GCTGATTTCT	ATGAAAGAGC	TGGAAAAGTT	GTGTGTTTAG	400
30	GAGACGATGA	AAGAGAAGGT	GCCATTACTG	CAATAGGTGC	TGTATC	446

2) INFORMATION FOR SEQ ID NO: 828

35

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 445 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

50	CAGCATCAGC	TTGCTAAATG	GGCAGATGCA	GATATAGTTG	TATATATAGG	50
	CTGTGGCGAG	CGTGGAATG	AAATGACAGA	TGTTCTTCTT	GAATTTCCTG	100
	AATTAAAAGA	CCCAAGAACA	GGCGAGTCAC	TTATGCAAAG	AACTGTGCTT	150
	ATAGCAAATA	CATCAGATAT	GCCGGTTGCT	GCACGTGAAG	CTTCTATATA	200
	CACTGGTATT	ACAATAGCTG	AATATTTTAG	AGATATGGGA	TATAGTGTTG	250
55	CACTTATGGC	AGACTCTACA	TCAAGATGGG	CTGAGGCTCT	TAGAGAGATG	300
	AGTGGTCGTT	TAGAGGAGAT	GCCTGGTGAA	GAAGGTTATC	CTGCATACTT	350
	AGGTTACAGT	CTTGCTCAAT	TCTATGAGAG	AGCAGGAAAG	GTAAATTGTC	400
	TAGGTATGGA	TGAAAGAGAA	GGAACACTTA	CAGCAATTGG	TGCAG	445

60

2) INFORMATION FOR SEQ ID NO: 829

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

ATGCTATAGC	TAAATGGGGA	GACAGCGAAA	TAGTTGTTTA	CGTTGGATGT	50
GGAGAACGTG	GTAACGAAAT	GACAGACGTT	CTTAACGAAT	TCCCAGAACT	100
TATTGACCCA	AAAACCTGGG	AAAGTTTAAT	GAAGAGACA	GTACTTATAG	150
CTAATACTTC	AAACATGCCA	GTTGCTGCTA	GAGAAGCTTG	CATATACACA	200
GGTATTACAA	TAGCTGAATA	CTTCAGAGAT	ATGGGATACT	CAGTATCTAT	250
AATGGCTGAT	TCAACTTCAA	GATGGGCAGA	AGCATTAAGA	GAAATGTCAG	300
GTAGACTTGA	AGAAATGCCA	GGTGATGAAG	GATATCCAGC	GTACTTAGGA	350
TCAAGACTTG	CTGATTATTA	CGAAAGAGCA	GGTAAGGTTG	TTTGTCTAGG	400
TAAAGATGGT	AGAGAAGGTG	CTGTAACAGC	AATTGGAGCT	GTATC	445

2) INFORMATION FOR SEQ ID NO: 830

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

TCAAATTGCT	AAATGGGGAG	ATGCAGAAAT	CGTTGTTTAC	GTTGGATGCG	50
GAGAACGTGG	TAACGAAATG	ACAGACGTTG	TTAATGAGTT	CCCAGAACTT	100
ATTGACCCTA	AGACTGGCGA	AAGCTTAATG	AAGAGAACAG	TTCTTATAGC	150
TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
GTATCACAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
AATGATGGAA	GAATTGTTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

2) INFORMATION FOR SEQ ID NO: 831

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: ATCC 13124

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTT	TTAACGAATT	100
15	CCCAGAACTT	AAAGACCCTA	AAACTGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
20	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
	TATCCC					456

25 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

40	CCAAGTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAACTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
45	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350
	CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
50	CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

2) INFORMATION FOR SEQ ID NO: 833

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

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10  TGAACCAAGG AAAAATAATA ACCGTTTCGG GACCTCTTGT TGTGGCTTCT 50
    GGGATGCAAG AAGCTAATAT TCAAGATATT TGTCGTGTGG GACATCTTGG 100
    CTTAGTCGGA GAAATTATTG AAATGCGTCG CGATCAAGCG TCTATTCAGG 150
    TTTATGAGGA AACATCAGGG ATCGGTCCAG GAGAACCAGT AGTGACTACT 200
    GGTGTGCCTT TGTCGGTCGA GTTAGGCCCG GGCCTGATT T CAGAAATGTT 250
    TGACGGTATT CAGCGACCGC TTGATCGTTT TCAAAAAGCA ACGGACAGCG 300
15  ACTTTTAAAT CCGTGGTGTG GCTATCCCAA GTCTTGATCG AAAGGCTAAG 350
    TGGGCATTTA TTCCAAGCT AAGTGTGGT CAAGAAGTAG TTGCAGGTGA 400
    TATTTTAGGA ACTGTGCAAG AAACAGCTGT CATTGAGCAC CGTATCATGG 450
    TTCCTTATAA AGTTTCAGGG ACCTTGGTGG CTATTCATGC AGGGGACTTC 500
    ACAGTAACAG ATACAGTTTA TGAAATTAAG CAGGAAGACG GTTCCATTTA 550
20  CCAAGGTAGC CTCATGCAGA CTTGGCCAGT TCGTCAAAGT CGCCCTGTTG 600
    CTCAAAGCT TATCCAGTC GAACCTTTGG TTACAGGTCA ACGGGTTATT 650
    GACACCTTTT TCCCTGTTAC AAAAGGTGGT GCCGCTGCCG TTCCTGACC 700
    ATTTGGGGCA GGAAAAACAG TTGTGCAGCA TCAATAGCT AAATTTGCCA 750
    ACGTTGATAT TGTTATTTAT GTCGGTTGTG GGAACGCGG CAACGAGATG 800
25  ACCGACGTTT TGAATGAGTT TCCAGAGTTA ATTGACCCAA ATACAGGCCA 850
    GTCCATTATG GAGCGCACGG TGTTAATTGC AAACACCTCT AATATGCCAG 900
    TAGCAGCGCG TGAAGCGTCG ATTTACACAG GTATTACCAT TGCCGAATAT 950
    TTCCGTGATA TGGGCTATTC TGTGGCTATC ATGGCAGACT CGACATCACG 1000
    TTGGGCAGAA GCTCTGCGCG AGATGTCAGG ACGCCTACAA GAAATGCCTG 1050
30  GTGATGAAGG CTACCCGGCT TACTTAGGGA GTCGTATTGC CGAATATTAT 1100
    GAACGGGCTG GTCGTGTTG GACCTTGGGA AGTCAAGAAC GTGAGGGAAC 1150
    CATTACAGCC ATCGGCGCGG TTTCTCCTCC TGGAGGGGAT ATTTTCAGAGC 1200
    CTGTCACTCA AAACACCCTT CGGATTGTCA AAGTTTTCTG GGGGCTCGAC 1250
    GCGCCTCTTG CGCAACGGCG TCACTTCCCA GCGATTAAC T GGCTGACGTC 1300
35  TTATTCATTG TATCAAGATG ATGTAGGAAG CTATATTGAC CGTAAACAGC 1350
    AATCTAATTG GTCCAACAAG GTAACTCGTG CCATGGCTAT TTTGCAGCGT 1400
    GAAGCCAGTC TAGAAGAAAT TGTACGCTTG GTGGGGCTTG ATTCACTGTC 1450
    TGAACAAGAT CGTTTGACCA TGGCTGTTGC CCGGCAAATT CGGGAGGATT 1500
    ATCTCCAGCA AAATGCCTTT GATTCGGTGG ATACCTTTAC TTCCTTTCCG 1550
40  AAACAAGAGG CCATGCTAAC CAATATTTTG ACCTTTAATG AGGAAGCCAG 1600
    CAAAGCCCTT TCTTTGGGAG CTTATTTTAA TGAGATTATG GAAGGCACTG 1650
    CTCAGGTACG CGATCGCATC GCACGCAGCA AATTTATCCC AGAAGAAAAC 1700
    TTAGAGCAGA TTAAAGGGCT TACTCAGAAG GTTACCAAAG AGATTCACCA 1750
    CGTTTTAGCA AAGGGAGGAA TTTAGATGAG CGTTCT 1786
45

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2) INFORMATION FOR SEQ ID NO: 834

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bovis*

(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

	TATCTCACGT	AAGTTTTTGC	GCGGCGGTTA	TATATCACTC	CAGGCCCTGG	50
5	CTAAGTACGC	TAATACTGAC	GTTACTGTCT	ATGTGGGATG	TGGAGAGCGT	100
	GGAAACGAGA	TTGCGGAGGT	GCTTAAGGAG	TTCCCTGAGC	TGAAGACCAA	150
	GGTTGATGGC	AAGGAAGTGA	GCATTATGAA	ACGCACTTGC	TTGGTGGCCA	200
	ATACTTCAAA	CATGCCAGTG	GCCGCCAGGG	AGGCTAGTAT	CTACACTGGC	250
	ATTACCCTAT	GTGAATACTT	CAGGGATATG	GGATAACAACG	CCTGTGTGAT	300
10	GGCGGATTCC	ACCAGTCGTT	GGGCTGAGGC	TTTGCCTGAG	ATATCAGGTC	350
	GTTTAGCTGA	GATGCCTGCT	GATTCAGGTT	ATCCCGCCTA	CCTTGCTTCT	400
	AGGCTTTCGG	CGTTCCTATGA	GCGTGCTGGT	ACAGCTGAGT	GTATTGGAAC	450
	ACCACTTCGT	GAAGGTTTCAG	TTACCATTGT	TGGTGCTGTA	TCTCCACCA	499

15

2) INFORMATION FOR SEQ ID NO: 835

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 464 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

	TTTCTCAAGC	TTTGAGTAAA	TATAGTAACT	CTGATGTTAT	TATTTACATT	50
	GGTTGTGGAG	AAAGAGGAAA	TGAAATGGCA	GAAGTTCTTA	CAGAATTCCC	100
	TGAGCTTTAT	ACTATGGTTG	ATGGAAAGAA	GGAGTCAATT	ATGCAAAGAA	150
35	CTTGTTTAGT	AGCTAATACA	TCAAATATGC	CTGTCGCTGC	TAGAGAAGCT	200
	TCCATCTACA	CTGGTATTAC	ACTTTCTGAA	TACTTTAGAG	ATATGGGATG	250
	TAATGTTTCT	ATGATGGCAG	ATTCAACTTC	TCGTTGGGCT	GAAGCTCTTA	300
	GAGAAATTTT	TGGTAGATTA	GCTGAAATGC	CTGCAGATTC	GGGTTACCCA	350
	GCATATTTAG	GCGCCAGACT	TGCTTCATTC	TATGAAAGAT	CAGGAAGAGT	400
40	TAAATGTATG	GGTTCCCCAG	ATAGAGAAGG	TACAGTAACA	ATTGTTGGTG	450
	CAGTTTCTCC	ACCT				464

45 2) INFORMATION FOR SEQ ID NO: 836

3)

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

60


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GCCCTCTCCA AGTACTCCAA CTCCGATTGC GTCATCTATG TCGGCTGCGG      50
CGAGCGCGGT AATGAGATGG CCGAGGTGCT CATGGAGTTC CCGACCCTGA      100
CGACCGTGAT CGATGGCCGC GAGGAGTCGA TCATGAAGCG CACCTGCCTC      150
GTGGCGAACA CCTCGAACAT GCCAGTCGCA GCGCGTGAGG CCTCTATTTA      200
5 CACCGGCATC ACCCTGGCCG AGTACTACCG TGATATGGGC AAGCATATCG      250
CCATGATGGC TGA CTGACG TCTCGCTGGG CCGAGGCGCT TCGTGAGATT      300
TCGGGTTCGTC TGGCGGAGAT GCCGGCGGAT GGTGGCTACC CCGCCTACCT      350
CAGCGCTCGT CTCGCCTCCT TCTACGAGCG CGCCGGCCTC GTCACCTGCA      400
TCGGCGGGCC GAAGCGCCAG GGCTCCGTCA CGATCGTCGG TGCCGT          446
10

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2) INFORMATION FOR SEQ ID NO: 837

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 25 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

```

TTAGTCAGGC CCTCTCCAAG TACTCCAACT CCGACTGCGT CATCTATGTC      50
30 GGCTGCGGCG AGCGCGGTAA TGAGATGGCT GAGGTGCTCA TGGATTTCCC      100
AACTCTGACG ACCGTGATCG ATGGTCGCGA GGAGTCCATC ATGAAGCGCA      150
CCTGCCTCGT GGCAACACT TCGAACATGC CAGTCGCAGC CCGCGAGGCC      200
TCTATTTACA CCGGCATCAC CCTGGCCGAG TACTACCGTG ATATGGGCAA      250
GCATATTGCC ATGATGGCCG ACTCGACATC TCGCTGGGCC GAGGCGCTTC      300
35 GTGAGATTTT CGGTCGTCTG GCGGAGATGC CAGCCGATGG TGGCTACCCT      350
GCCTACCTCA GCGCTCGTCT CGCCTCCTTC TACGAGCGCG CCGGCCTCGT      400
CACCTGCATC GCGGGGCCGA AGCGCCAGGG CTCCGTCACG ATCGTCGGTG      450
CTGTGT          456
40

```

2) INFORMATION FOR SEQ ID NO: 838

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 55 (B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

```

AGGCCCTCTC CAAGTACTCC AACTCCGACT GCGTCATCTA CGTCGGCTGC      50
GGCGAGCGCG GTAATGAGAT GGCCGAGGTG CTCATGGAGT TCCCGACCCT      100
60 GACGACTGTG ATTGATGGCC GTGAGGAGTC GATCATGAAG CGGACCTGCC      150

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	TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
	TACACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
	CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
	TTTCGGGTCG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
5	CTTAGTGCTC	GTCTTGCCCTC	CTTCTACGAG	CGTGCCGGCC	TCGTCACCTG	400
	CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

10 2) INFORMATION FOR SEQ ID NO: 839

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

25	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGGC	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
30	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCGCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGGTGGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
35	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

2) INFORMATION FOR SEQ ID NO: 840

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 50 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
55	TTCGAGTCGC	CCAAGTCTGT	GTTCACGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
60	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350

	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
5	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCG	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCG	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
10	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTC	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
15	CC					1052

2) INFORMATION FOR SEQ ID NO: 841

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

35	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTCGAGTCGC	CCAAGTCTGT	GTTACAGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
40	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
45	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCG	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCG	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
50	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
55	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

2) INFORMATION FOR SEQ ID NO: 842

470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

```

15 GCTGAAGGCT GAGCGCGAGC GCGGCATCAC GATCGACATC GCGCTCTGGA      50
   AGTTCGAGTC GCCCAAGTCT GTGTTTCACGA TCATCGACGC CCCC GGCCAC      100
   CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCTCAGG CGGACGCCGC      150
   CGTCCTTGTC ATTGCGTCAT CGCAGGGTGA GTTTGAGGCG GGCATCTCGA      200
20 AGGACGGCCA GACACGCGAG CACGCGCTGC TCGCCTTCAC GCTCGGCGTG      250
   AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGT CGGTGAAGTT      300
   CGCCCAGGAG CGCTACGATG AGATTGTGAA GGAGGTGTCT GCGTACCTGA      350
   AGAAGGTTGG GTACAACGTG GAGAAGGTGC GCTTCATCCC CATCTCCGGC      400
   TGGCAGGGCG ACAACATGAT TGACAAGTCG GAAAATATGC CGTGGTACAA      450
25 GGGCCCCACG CTGCTGGAGG CACTCGACAT GCTGGAGCCC CCGGTGCGCC      500
   CCAGCGACAA GCCGCTGCGC CTGCCGCTGC AGGACGTGTA CAAGATCGGC      550
   GGTATCGGCA CCGTGCCGGT CGGTCGCGTG GAGACGGGCA CGATGAAGCC      600
   CGGCGACGTG GTGACGTTTG CGCCCGCCAA CGTGACGACG GAGGTGAAGT      650
   CGATTGAGAT GCACCACGAG CAGCTGGCCG AGGCCACGCC CGGCGACAAC      700
30 GTCGGCTTCA ACGTGAAGAA CGTGTCGTG AAGGACATCC GCCGTGGCAA      750
   CGTGTGCGGC AACTCGAAGA ACGACCCCCC AAAGGAGGCG GCCGACTTCA      800
   CGGCGCAGGT GATCATCCTG AACCACCCCG GCCAGATCGG CAACGGCTAT      850
   GCGCCGCTGC TCGACTGCCA CACCTGCCAC ATCGCGTGCA AGTTCGCCGA      900
   GATCGAGTCC AAGATCGACC GCCGCTCCGG CAAGGAGCTT GAGAAGAACC      950
35 CCAAGTCGAT CAAGTCCGGT GACGCCGCCA TGGTGCGCAT GGTGCCGCAG      1000
   AAGCCCATGT GCGTGGAGGT GTTCAACGAC TACGCTCCTC TTGGCCGCTT      1050
   TGCCGTGCGT GA                                     1062

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2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

```

TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCATGGCG      50
AGTACACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT      100
GGTATTACTA TAAATTCGAC ACATGTTGAA TATGAGACTA AGAACCGTCA      150
60 TTACGGTCAC GTGGACTGTC CAGGTCACCT TGATTATGTG AAGAACATGA      200

```

	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTGTT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTCGTGA	GTTATTGAGT	400
5	GAGTTTGGTT	ACGACGGTGA	CAACACGCCT	ATCGTTCGTG	GCAGTGCTAT	450
	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTC	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTCGT	TGTGGTGACC	650
10	CTATTGAGGT	TTGCGCCGGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750
	GATTGGTGTT	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGCGCGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTTGATGCT	850
	GACTTGATAC	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
15	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

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2) INFORMATION FOR SEQ ID NO: 844

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*

(B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
40	TTCATCAACA	AAGTGGATAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
45	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCAACAAG	500
	CGCTGAGCGA	GTGCATGCCG	GGTGACTCCG	TCGGCGTCAG	CATTGTCGGC	550
	ACCGGCGACA	CAACCAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
50	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGGGA	GGAGCTGAAC	AAGAAATTCG	800
	GCCGCGGCCG	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
55	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTCGCGTAC	CCGATGCCCA	TTGAAAAGGG	CCTGAAGTTC	ACC	943

60 2) INFORMATION FOR SEQ ID NO: 845

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

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CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
GCGAGCATCT CTTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
CATGGAGGTG CGTGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAAGAGA      200
CGCCCATCGT GCGCGGCTCG GCCCTCAAAG CCGTCGAGGG CGACGCGAAG      250
TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AATGGATCCC      300
CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATTGAGCACG      350
TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
GATCAGGGCG TGCTGAAGCT CAACACAGAC GCCGAGCTGG CCGGCTTCAG      450
CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA      500
CGCTGAGTGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCCGG      550
ACCGGCGACA CGATCAGTCT CTCCAAGGAC AACGTTGAAC GCGGCATGGT      600
AATGGCGGCA ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650
TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCCACTGG CTTCAGCCCC      700
CACTACCGCC CGCAGCTCTT CTTCCATTGT GCTGACGTGA CGGCGGACAT      750
GAGCTTCCCG GAGGCGGAGA AGCACCGCGA GGAGCTCAAC AAGAAATTCTG      800
GCCGCGGCCC CGAGGAGGAC AAGCAGAAGG AGGCGGAGAT GAAAGAGTTC      850
GAGAGCAAGC TCGTCTGCAT GCCGGGCGAC AACC GCGAGC TGATCCTGAC      900
GCTGGCGTAC CCGATGCCCA TTGACAAGGG TCTGAAGTT      939

```

2) INFORMATION FOR SEQ ID NO: 846

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

```

CATTGTGGTG GCGGCCACCG ACGGCGTCAT GCCGCAGACA CGCGAGCACC      50
TCCTGATCTG CTCGCAGATC GGGCTTCCGG CGCTCGTAGG GTTCATCAAC      100
AAGGTGGACA TGACGGACGA GGACACGTGC GACCTGGTGG ACATGGAGCT      150
GCGCGAGCAG CTGGAGAAAT ACAAGTTTCC GGCGGAGGAG ACGCCAATCG      200
TGCGCGGCTC AGCCCTCAAA GCCGTCGAGG GCGATGCGAA GTACGAGGAG      250
AACATTCTCG AACTGGTGCG GAAGTGTGAC GAGTGGATCC CTGACCCGCC      300
GCGCAACACA GACAAGCCTT TCCTTATGGC CATCGAGCAC GTTTACGAGA      350

```

	TCGGCAAGGA	CAAGAAGAGC	GTTGTCTGTA	CCGGCCGCGT	CGATCAAGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTCGACGGTG	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCATGCC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCGG	GACCGGCGAC	550
5	ACGACCAGTC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
	GACGGGTAGC	ACGAACCTGT	ACAACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCACTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACCGCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
10	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900
	CCCGATGCC	ATTGAAAAGG	GTCTGAAGTT	CACCATCCGT	GAGGG	945

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2) INFORMATION FOR SEQ ID NO: 847

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania infantum*
 - (B) STRAIN: MOU

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	GCACCTCCTG	ATCTGCTCGC	AGATCGGGCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAGGT	GGACATGACG	GACGAGGACA	CGTGCGACCT	GGTGGACATG	150
35	GAGCTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACGCC	200
	AATCGTGCGC	GGCTCAGCCC	TCAAAGCCGT	CGAGGGCGAT	GCGAAGTACG	250
	AGGAGAACAT	TCTCGAACTG	GTGCGGAAGT	GTGACGAGTG	GATCCCTGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTTGT	CGTGACCGGC	CGCGTCGATC	400
40	AGGGCGTTCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCTCC	450
	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATC	GAGATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCTGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTATCC	AAGGGCAACG	TGGAACGCGG	CATGGTGATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
45	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTT	AGTCCTCACT	700
	ACCGCCCGCA	GCTCTTCTTC	CATTGTGCTG	ACGTGACGGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAAGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	AGCGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
50	GCGTACCCGA	TGCCCATTTGA	AAAGGGTCTG	AAGTTCACC		939

55

2) INFORMATION FOR SEQ ID NO: 848

60

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 933 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

```

10 CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC      50
   AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG      100
   GACGAGGATA CGTGCGACCT CGTGGACATG GAGGTGCGGG AACAGCTGGA      150
   GAAGTACAAG TTTCCGGCCG AGGAGACGCC CATCGTACGT GGCTCGGCCC      200
   TCAAGGCCCT CGAGGGGGAT GCGCAATACG AGGGGAGTAT TCTCGAGCTG      250
15 GTGCGAAAGT GCGACGAGTG GATCCCCGAC CCGCCGCGCA ACACCGAAAA      300
   GCCTTTCCTC ATGGCTATCG AGCACGTTTA CGAGCTCGGC AAAGACAAGA      350
   AGAGCGTCAT CGTTACCGGC CGCGTCGATC AAGGTGTGCT GAAGCTCAAC      400
   ACAGACGCCG AGCTGGCCGG CTTACGCGCC AAGAAGGCGA CAGTCAAAGT      450
   GACGGGCATC GAGATGTATC ACAAGACACT CAATGAGTGC ATGCCCGGCG      500
20 ACTCTGTCTG TGTCAGCATC GTCGGTACCG GTGACACGAC CAGCTTATCC      550
   AAGGATAATG TTGAGCGCGG TATGGTAATG GCGCAACGG GTAGCACGAA      600
   CCTGTACAAC AAGCTGAAGG CGCAGGTTTA CGTGCTGACA AAGGAGGAGG      650
   GTGGCCGCCA CACCGGGTTC AGCCCCACT ACCGCCCGCA GCTCTTCTTC      700
   CACTGCGCTG ACGTGACCGC AGACATGAGC TTCCCGGAGG CGGAGAAGTA      750
25 CCGCGAGGAG CTCAACAAGA AGTTCGGCCG TGGCCCTGAG GAGGACAAGA      800
   AGAAAGAGGC GGAGATGAAG GAGTTCGAAA GCAAACCTTG CTGCATGCCA      850
   GGCATAACC GCGAGCTGAT CCTAACTCTG GCGTACCCGA TGCCCATCGA      900
   CAAGGGCCTG AAGTTCACCA TCCGTGAGGG CGG                      933

```

30

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 943 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
45 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

```

CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
50 TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
   CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA      200
   CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACCGCAAG      250
   TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AGTGGATCCC      300
   CGACCCGCCG CGCAACACAG ACAAGCCTTT CTTATGGCC ATCGAGCACG      350
55 TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
   GATCAGGGCG TGCTGAAGCT CAACACGGAC GCCGAGCTGG CCGGCTTCAG      450
   CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATTGAGATG TACCACAAGA      500
   CGCTGAGCGA GTGCATGCCG GGTGACTCCG TCGGCGTCAG CATTGTCGGC      550
   ACCGGCGACA CGACCACTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT      600
60 AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650

```


	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGSCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
5	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

10 2) INFORMATION FOR SEQ ID NO: 850

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

25	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	ACACCTCCTG	ATCTGCTCGC	AAATTGGCCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAAGT	GGACATGACG	GACGAGGACA	CGTGTGACCT	GGTGGACATG	150
	GAGGTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACACC	200
30	AATCGTGCGC	GGCTCGGCCC	TCAAGGCCGT	CGAGGGCGAC	GCGAAGTACG	250
	AGGAGAACAT	CCTCGAACTG	GTGCGGAAGT	GCGACGAGTG	GATCCCCGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTCAT	CGTGACCGGC	CGCGTCGATC	400
	AGGGCGTGCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCCG	CTTCAGCGCC	450
35	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATT	GAAATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCCGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTGTCC	AAGGACAACG	TGGAGCGCGG	CATGGTAATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTC	AGCCCCCACT	700
40	ACCGCCCGCA	GCTCTTCTTC	CATTGCGCTG	ACGTGACAGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAGGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
45	GCGTACCCGA	TGCCCATT				918

2) INFORMATION FOR SEQ ID NO: 851

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 60 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
5	GCGAGCATCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGG	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTGAGGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AATGGATCCC	300
10	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGTCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGC	550
15	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACC CGCA	GGAGCTCAAC	AAGAAATTCG	800
20	GCCGCGGCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAGAAGGG	TCTGAAGTT		939

25

2) INFORMATION FOR SEQ ID NO: 852

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 912 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: MOU-2

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

	TCATTGTGGT	GGCCGCCACC	GACGGCGTCA	TGCCGCAAAC	ACGGGAGCAC	50
	CTTTTGATCT	GCTCGCAGAT	CGGGCTGCCG	GCGCTCGTAG	GGTTCATCAA	100
	CAAAGTGGAC	ATGACAGACG	AAGACACGTG	CGACCTGGTA	GACCTGGAGG	150
45	TGCGTGAGCA	GCTGGAGAAG	TACAAGTTTC	CGGCAGAGGA	AACACCAATC	200
	GTGCGTGGCT	CGGCCCTCAA	GGCCGTTGAG	GGCGATGCAA	AGTACGAGGA	250
	GAACATCCTC	GAACCTGGTG	GGAAGTGCGA	CGAGTGGATC	CCAGACCCGC	300
	CACGCAATAC	GGACAAGCCT	TTCCTTATGG	CCATTGAACA	CGTGTACGAG	350
	ATCGGCAAGG	ATAGGAAAAG	CGTCATCGTA	ACCGGCCGCG	TCGATCAAGG	400
50	TGTGCTGAAG	CTGAACACAG	ACGCCGAGCT	GGCCGGCTTC	AGCGCCAAGA	450
	AGTCGACGGT	GAAAGTGACG	GGCATTGAGA	TGTACCACAA	GACACTGACA	500
	GAGTGCATGC	CCGGCGACTC	TGTCGGCGTC	AGCATTGTGG	GCACTGGYGA	550
	CACGACCAGC	CTCTCTAAGG	ACAATGTTGA	GCGTGGCATG	GTA CTGGCCG	600
	CTACGGGTAG	CACGAACCTG	TACAACAAAG	TAAAGGCGCA	GGTGTATGTA	650
55	CTCACGAAGG	ATGAGGGCGG	CCGCCACACC	GGCTTCAGCC	CCCACTACCG	700
	TCCGCAGCTC	TTCTTCCACT	GCGCTGACGT	AACGGCGGAC	ATGAGCTTCC	750
	CGGAGGCGGA	GAAGCACCGC	GAGGAACTCA	ATAAGAAATT	CGGCCGCGGC	800
	CCCAGAGGAG	ACAAGAAAAA	GGAGGCGGAG	ATGAAGGAGT	TCGAGAGCAA	850
	GCTGGTCTGC	ATGCCAGGCG	ATAACCGCGA	GCTGATCCTG	ACATTGGCGT	900
60	ACCCGATGCC	TA				912

2) INFORMATION FOR SEQ ID NO: 853

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

```

20  ATTCTTGTGG TGGCAGCTAA CGACGGATGC ATGCCGCAGA CGCGTGAGCA      50
    CCTGCTTATT TGTTTCGAGA TTGGCCTTCC TGCTCTTGTA TGCTTTATCA      100
    ATAAGTGTGA CATGATGCAA GGGCAGGAGG AAATGATTGA ACTTGTTGAA      150
    ATGGAGGTAC GTGAACCTTT GGAGAAGTAC AAGTTCCTTG CGGAGGAGAC      200
    GCCATTTGTG CGGGGGTCTG CGGTGAAGGC ATTGGAGGGT GATGCTGAAA      250
25  ATGAAGGAAA GATTTTGGAG CTTGTAAAAA AATGTGATGA ATGGATTCCC      300
    GACCCACCGC GTGCCATTGA AAAACCGTTC CTTATGGCCA TTGAGCACGT      350
    TTTTGAGGTT GGAAAGGATA AGAAGGCCGT TGTGTGAGC GGGCGTGTGG      400
    ACCAGGGGCA GTTGAAGGTC GCGCGAGATG CAGAACTTTC CGGGTTTAGC      450
    GCAAAGAAGC TGACGGTGAA GGTGCTAGC ATCGAAATGT ACCATAAAAT      500
30  TCTGGAGGAT TGCATGCCTG GTGACTCTGT TGGCGGAAG ATCGTTGGCA      550
    GCGGTGAAAC AGTGAACCTG TCGAAGGAAA ATGTGGAACG CGGCATGGTA      600
    CTCTCCGCAC CAGGTGCAAC GACACTGTTT AACAAAGGTCC GCGCGCAGGT      650
    GTACGTGTTG ACAAAGGAAG AAGGCGGTCG TCACACAGCC TTAGTCCTC      700
    ACTATCGTCC GCAGCTTTTC TTCCACTGTG CTGATGTCAC GGCAGATATT      750
35  AACTTCCCGG AAAGCGAGAA GCTTGCAGGG GAGCTGAACA AAAAGTATGG      800
    CCGTGATGCG GCGGAACAGA AGAAGAAGGA GGCAGAACTG AAAGAGTTTG      850
    AAAAGACGCT TGTCTGCATG CCTGGTGATA ACCGCGAACT CCTGCTCACC      900
    CTTGCCTATC CAATGCCAAT GGAAAAGGGA CTCAAG                      936

```

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

```

CGGCATTCTT GTGGTGGCAG CTAACGACGG ATGCATGCCG CAGACGCGTG      50
AGCACCTGCT TATTTGTTTC GAGATTGGCC TTCCTGCTCT TGTATGCTTT      100
60  ATCAATAAGT GTGACATGAT GCAAGGGCAG GAGGAAATGA TTGAGCTTGT      150

```

	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCGACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCCCTTATG	GCCATTGAGC	350
5	ACGTTTTTTGA	GGTTGGAAAG	GATAAGAAGG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTTGC	TAGCATCGAA	ATGTACCATA	500
	AAATTCTGGA	GGATTGCATG	CCTGGTGACT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTGGAAG	GAAAAATGTG	AACGCGGCAT	600
10	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAAC TTC	CCGGAAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
15	TTTGAAAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGA		934

20 2) INFORMATION FOR SEQ ID NO: 855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

35	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGG	GAAGTACAAG	TTCCCTGCGG	200
40	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAaaaaaat	GTGATGAATG	300
	GATTCCCGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
	AGCACGTTTT	TGAGGTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACTTTCGGG	450
45	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTCTG	AAGGAAAATG	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTCGTCA	CACAGCCTTT	700
50	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
55	GCTCACCCCTT	GCCTATCCAA	TGCCAATGGA	AAAGGA		937

2) INFORMATION FOR SEQ ID NO: 856

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

15	CTTATTATGG	AGCTGATCAA	CAACGTCGCG	AAGAAGCACG	GTGGTTTCTC	50
	CGTGTTTCGCC	GGCGTCGGCG	AGCGCACCAG	GGAGGGCAAC	GAGCTGTACC	100
	ACGAGATGAT	GGAGACCGGC	GTCATCAAGC	GCCGCCAGCT	GGATGACGGC	150
	ACGTTTCGACT	TCTCCGGCTC	CAAGGCCGCG	CTGGTGTACG	GCCAGATGAA	200
	CGAGCCGCCA	GGTGCCAGGG	CGCGTGTTGC	CCTCACTGGC	CTGACGGTGG	250
	CCGAGTACTT	CCGTGATGAG	GACGGCCAGG	ACGTGCTGCT	CTTCATCGAC	300
20	AACATCTACC	GTTTCACCCA	GGCTGTTTCT	GAGGTGAGTG	CCCTTTTGGG	350
	GCGCATCCCG	TCCGCCGTCG	GTTACCAGCC	GACCCTCGCC	ACCGACCTTG	400
	GCGCGCTGCA	GGAGCGTATC	ACGACGACCA	ACAAGGGCTC	CATCACCTCC	450
	GTGCAGGCCG	TCTACGTGCC	GGCCGACGAT	ATCACCGACC	CGGCGCCTGC	500
	GACCACCTTC	ACCCATCTGG	ACGCGACCAC	TGTGCTCTCC	CGTTCCATCG	550
25	CCGAGCTGGG	TATCTACCCC	GCCGTCGACC	CGCTCGACTC	CACCTCGCGT	600
	ATGCTGTCCG	CGAACATCGT	CGGCGAGGAG	CAGTACAACG	TGGCGCGTGG	650
	CGTGCAGAAA	ATACTGCAGG	ACTACAAATC	GCTGCAGGAT	ATCATCGCCA	700
	TCCTGGGTAT	GGACGAGCTG	TCTGAGCAGG	ACAAGTTCGT	CGTCGCGCGT	750
	GCGCGCAAGG	TTCAGCGTTT	CCTATCCAG	CCCTTCCAGG	TGGCTGAGGT	800
30	ATTCACCGGC	AAGCCCGGAC	GTTTCGTCGA	GCTGCAGGAC	ACCATCAGCG	850
	GCGTCAAGGA	GATTTTGGAC	GGCGAGTGCG	ACGACATG		888

35 2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

50

55	TGATTATGGA	ATTGATCAAC	AATGTCGCCA	AGAAACACGG	TGGGTTCTCC	50
	GTGTTTCGCTG	GTGTTGGTGA	ACGTACGAGG	GAAGGTAACG	AACTGTACCA	100
	TGAAATGATG	GAAACGGGTG	TCATCAAGCG	CCGTCAACTG	GAAGACGGAA	150
	CATTTGACTT	CTCGGGCTCT	AAAGCTGCTT	TGGTGTACGG	ACAAATGAAC	200
55	GAACCACCAG	GTGCTAGAGC	CCGTGTTGCA	CTCACGGGAT	TGACCGTTGC	250
	CGAGTATTTT	CGTGATGAAG	AGGGGCAGGA	TGTGCTACTC	TTCATCGATA	300
	ACATCTACCG	TTTCACCCAG	GCCGGTTCCG	AAGTGAGTGC	GCTGTTAGGA	350
	AGAATTCCAT	CCGCCGTGGG	TTATCAACCT	ACATTGGCCA	CTGATCTCGG	400
	AGCACTCCAG	GAACGCATTA	CTACAACCAA	CAAGGGTTTCG	ATTACATCAG	450
60	TCCAGGCAGT	ATACGTCCCA	GCCGATGATA	TCACTGATCC	CGCTCCAGCT	500

ACCACTTTCT	CGCACTTGGG	TGCCACTACA	GTGCTTTCTC	GTTCAATTGC	550
GGAGTTGGGT	ATTTACCCTG	CGGTCGACCC	GCTTGACTCA	ACGTCACGTA	600
TGCTGTCGGC	CAACATTGTA	GGACAGGAAC	AGTACGATGC	CGCACGTGGT	650
GTACAGAAAA	TTTTACAGGA	CTACAAATCA	CTGCAGGATA	TCATTGCCAT	700
5 TCTGGGTATG	GACGAGCTGT	CTGAGCAGGA	CAAGTTCGTT	GTAGCACGCG	750
CCCCTAAGGT	ACAGCGTTTC	CTGTCTCAGC	CGTTCCAAGT	GGCTGAGGTG	800
TTCACCGGCA	AGCCTGGGAG	GTTCGTTGAA	CTACAGGATA	CCATCAGCGG	850
TGTCAAGGAA	ATCTGGAAGG	TGAGTGTGAC	GATA		884

10

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

TGGAAGTAT	TAATAATGTG	GCCAAAAAGC	ATGGCGGTTA	CTCTGTTTTT	50
GCAGGTGTAG	GTGAAAGGAC	GAGGGAGGGT	AATGAATTGT	ACCATGAAAT	100
30 GATGGAGACA	GGTGTATATA	AGAAAAAGGC	ACTAGGTGGT	GGGAAGTTTG	150
ATTTCAAGTG	ATCTAAAGCA	GCGCTGGTCT	ATGGACAAAT	GAACGAGCCA	200
CCTGGGGCCC	GTGCTAGAGT	GGCACTAACT	GGATTAACAG	TCGCAGAATA	250
TTTCCGTGAC	GAACAAGGAC	AAGACGTGTT	GTTGTTTATT	GATAATATTT	300
ACCGATTTAC	TCAGGCAGGG	TCTGAGGTTT	CAGCCTTGCT	AGGCCGTATA	350
35 CCTTCAGCTG	TGGGATACCA	GCCTACATTG	GCAACAGATC	TTGGCTGTTT	400
ACAAGAACGA	ATTACTACGA	CCAAATCTGG	TTCAATCACC	AGTGTTACAAG	450
CTGTGTATGT	GCCAGCAGAT	GATATTACTG	ATCCAGCGCC	TGCCACAACCT	500
TTTACTCACT	TGGACGCTAC	TACTGTACTT	AGCAGGCCAA	TTGCTGAACT	550
CGGTATTTAT	CCAGCGGTAG	ACCCGTTGGA	TTCAACAAGC	CGTATGCTAA	600
40 GCGCGAACAT	TGTGGGAAAT	GAACACTATA	GTGTAGCCCG	TTCCGTGCAG	650
AAGATACTGC	AAGATTACAA	ATCGCTTCAG	GACATTATTG	CCATTTTGGG	700
TATGGATGAA	CTGTCGGAAC	AAGACAAAAA	TATAGTAGCC	CGAGCAAGGA	750
AGATGCAAAG	GTTCTTATCA	CAGCCATTCC	AAGTGCGCGA	AGTTTTTACT	800
GGTAAACCGG	GAAGATTGTG	GGAATTGGAA	GATACAATTG	CCGGGGCACG	850
45 AGATATAATT	GCGGGTAATT	G			871

2) INFORMATION FOR SEQ ID NO: 859

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Leishmania guyanensis*

481

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

5	TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
	CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
	GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
	GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
	GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
10	CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
	ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
	TGCAAGGGCG	GCAAGATCGG	CCTGTTCGGC	GGTGCCGGTG	TGGGCAAGAC	400
	TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
	TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
15	TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
	GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
	GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
	GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
	GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
20	ACCAGCCGAC	GCTTGCGGAG	GATCTTGCA	TGCTGCAGGA	GCGCATTACG	800
	TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
	GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
	CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
	GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
25	CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
	ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
	GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCTT	1150
	GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
	ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
30	TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 860

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

50	CTCGGAGGGC	GTCCCGCCCG	TGCTGACGGC	GCTGGATGTG	ACGGAGGACC	50
	TTGGCCGCGA	TGAGCCGCTG	ACGCTGGAGA	TCGTGCAGCA	CCTGGACGCG	100
	AACACCGGCC	GCTGCATTGC	GATGCAGACG	ACGGACCTGC	TGAAGCTGAA	150
	GTCGAAGGTT	GTGTGACCCG	GCGGCAACAT	CTCTGTGCCG	GTGGGCCGTG	200
	AGACGCTGGG	CCGCATCTTC	AACGTGCTGG	GCGACGCGAT	CGACCAGCGC	250
55	GGCCCCGTGG	GTGAGAAGAT	GCGCATGGCG	ATCCACGCCG	AGGCCCCGAA	300
	GCTGGCGGAT	CAGGCCGCGG	AGGACACGAT	CCTGACGACC	GGCATCAAGG	350
	TGATCGACCT	GATTCTGCCC	TACTGCAAGG	GTGGCAAGAT	CGGCCTGTTT	400
	GGCGGCGCCG	GTGTGGGCAA	GACCGTGATC	ATCATGGAGC	TGATTAACAA	450
	CGTCGCGAAG	GGCCACGGTG	GTTTCTCGGT	GTTTGCCGGC	GTTGGCGAGC	500
60	GCACGCGCGA	GGGCACGGAC	CTGTACCTGG	AGATGATGCA	GTCGAAGGTG	550

	ATTGACCTGA	AGGGCGAGTC	GAAGTGCCTG	CTTGTGTACG	GGCAGATGAA	600
	CGAGCCCCCG	GGTGCGCGCG	CGCGCGTTGC	GCAGTCTGCG	CTGACGATGG	650
	CGGAGTACTT	CCGAGACGTG	GAGGGCCAGA	ATGTGCTGCT	GTTTCATCGAC	700
	AACATCTTCC	GCTTCACGCA	GGCGAACTCC	GAGGTCTCTG	CGCTGCTGGG	750
5	CCGCATTCCG	GCCGCCGTGG	GCTACCAGCC	GACGCTTGCG	GAGGATCTTG	800
	GTATGCTGCA	GGAGCGCATC	ACGTCGACGA	CGAAGGGGTC	GATCACGTCC	850
	GTGCAGGCCG	TGTACGTGCC	TGCGGATGAT	ATCACGGATC	CGGCGCCCCG	900
	GACGACGTTT	TCGCACCTGG	ACGCGACGAC	TGTGCTGGAC	CGCGCGGTGG	950
	CGGAGTCGGG	GATCTACCCT	GCCGTGAACC	CGCTGGAGTG	CGCGTCGCGT	1000
10	ATCATGGACC	CCGATGTGAT	CGACGTGGAC	CACTACAACG	TTGCGCAGGA	1050
	TATCGTGACG	ATGCTGACCA	AGTACAAGGA	GCTGCAGGAT	ATCATTGCGG	1100
	TGCTTGGTAT	CGACGAGCTG	AGCGAGGAGG	ACAAGGTCGT	GGTGGACCGC	1150
	GCGCGCAAGG	TGACCCGGTT	CCTGTGCGAG	CCGTTCCAGG	TTGCGGAGGT	1200
	GTTTCACGGG	ATGACGGGCC	AC			1222

2) INFORMATION FOR SEQ ID NO: 861

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1246 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tropica*
 - (B) STRAIN: ATCC 50129
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGCCCG	CGATGAGCCG	50
35	CTGACGCTGG	AGATCGTGCA	GCACTTGAC	GCGAACACCG	GCCGCTGCAT	100
	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	GTTGTGTGCA	150
	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	GGGCCGCGATC	200
	TTCAACGTTT	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	TGGGCGAGAA	250
	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	GATCAGGCCG	300
40	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	CCTGATTCTG	350
	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	CCGGTGTGGG	400
	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	AAGGGCCACG	450
	GTGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	CGAGGGCACG	500
	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	TGAAGGGCGA	550
45	GTCGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	GAACGAGCCC	CCGGGTGCGC	600
	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	CTTCCGCGAC	650
	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACTCT	TCCGCTTCAC	700
	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCGATT	CCGGCCGCCG	750
	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	GCAGGAGCGC	800
50	ATCACGTGCA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	CCGTGTACGT	850
	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	TTCTCGCACC	900
	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	GGGCATCTAC	950
	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	ACCCCGATGT	1000
	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	CAGATGCTGA	1050
55	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	CATCGACGAG	1100
	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	AGGTGACCCG	1150
	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	GGTGTTCACG	GGCATGACGG	1200
	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	TGGCCT	1246

2) INFORMATION FOR SEQ ID NO: 862

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1265 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30815

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	50
	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACGG	100
20	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	150
	GTCGTGTCTGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	200
	GGGCCGCATC	TTCAAYGTTT	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	250
	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	300
	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	350
25	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	400
	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	450
	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	500
	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	550
	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	GAACGAGCCC	600
30	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	650
	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	GACAACATCT	700
	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	750
	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	800
	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	850
35	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	900
	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	950
	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	1000
	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	1050
	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	1100
40	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	1150
	AGGTGACCCG	GTTCTGTCTG	CAGCCGTTCC	AGGTTGCGGA	GGTGTTTACG	1200
	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	1250
	TGGCCTGCTG	ATGGG				1265

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2) INFORMATION FOR SEQ ID NO: 863

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1191 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

	ATGGCAAAG	GCAAGTTTGA	ACGTACCAAG	CCGCACGTGA	ACGTGGGTAC	50
	GATTGGTCAC	GTTGACCACG	GCAAAACGAC	GTTGACGGCG	GCGATCACGA	100
	CGGTGCTGTC	GAACAAGTTC	GGCGGCGAGG	CTCGCGGCTA	CGACCAGATT	150
5	GACGCGGCGC	CGGAAGAGAA	GGCGCGTGCG	ATCACGATCA	ACACCTCGCA	200
	CGTTGAGTAC	GAGACGGAGA	CGCGTCACTA	CGCGCACGTT	GATTGCCCGG	250
	GTCACGCTGA	CTACGTGAAG	AACATGATCA	CGGGTGCTGC	GCAGATGGAC	300
	GGCGCGATCC	TGGTGGTGTC	GGCCGCAGAC	GGCCCGATGC	CGCAGACGCG	350
	CGAGCACATT	TTGCTGTCGC	GCCAGGTTGG	CGTGCCGTAC	ATCATCGTGT	400
10	TCCTGAACAA	GGCGGACATG	GTTGATGACG	CGGAGCTGCT	CGAGCTGGTG	450
	GAGATGGAAG	TCCGCGAACT	GCTGAGCAAG	TACGATTTCC	CGGGCGATGA	500
	CACGCCGATC	GTGAATGGTG	CGGCCAAGCT	GGCGCTGGAA	AGCGACAACG	550
	GCGACCTGGG	CGAGCAGGCG	ATTCTGTCGC	TGGCGCAAGC	GCTGGACACG	600
	TACATTCCGA	CGCCGAGCG	CGCGGTCGAC	GGTGCGTTCC	TGATGCCGGT	650
15	GGAAGACGTG	TTCTCGATCT	CGGGCCGTGG	CACGGTGGTG	ACTGGCCGTA	700
	TCGAGCGCGG	CGTGGTGAAG	GTTGGCGAGG	AAATCGAAAT	CGTGGGCATC	750
	AAGCCGACGG	TGAAGACGAC	CTGCACGGGC	GTGGAGATGT	TCCGCAAGCT	800
	GCTGGACCAG	GGCCAGGCGG	GCGACAACGT	GGGTATCTTG	CTGCGCGGCA	850
	CCAAGCGTGA	AGACGTCGAG	CGTGGCCAGG	TGCTGGCCAA	GCCGGGTTCG	900
20	ATCAACCCGC	ACACGGACTT	CACGGCCGAG	GTGTACATTC	TGTCCAAGGA	950
	AGAGGGTGGC	CGTCACACGC	CGTTCTTCAA	CGGCTATCGT	CCGCAGTTCT	1000
	ACTTCCGCAC	GACGGACGTG	ACCGGCACGA	TCGACCTGCC	GGCGGACAAG	1050
	GAAATGGTGC	TGCCGGGCGA	CAACGTGTCG	ATGACCGTCA	AGCTGCTGGC	1100
	CCCGATCGCC	ATGGAAGAAG	GTCTGCGTTT	CGCCATCCGT	GAAGGCGGTC	1150
25	GTACCGTCGG	TGCCGGCGTC	GTCGCCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 864

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1350 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Trypanosoma brucei*
- (B) STRAIN: LVH/75/USAMRU-K/18
- (C) ACCESSION NUMBER: extracted from U10562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

45

	ATGGGAAAGG	AAAAGGTGCA	CATGAATCTT	GTGGTGGTGG	GCCACGTGCA	50
	TGCCGGTAAA	TCCACTGCAA	CGGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
	TTGACAAACG	TACGATCGAG	AAGTTCGAGA	AAGAAGCTGC	CGACATTGGT	150
	AAGGCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
50	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CACTATTATT	GATGCTCCTG	GGCACCCTGA	CTTCATCAAG	300
	AACATGATCA	CCGGCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTGC	350
	CTCTGCGCAG	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCACTTTGG	GTGTGAAGCA	GATGGTTGTG	450
55	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCAGT	GCGTCCGAGC	GACAAGCCCC	700
60	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TCGGTGGTAT	TGGCACCGTG	750

	CCCGTTGGTC	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGYGAC	800
	GTTTGCCCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
	ACGAGCAGCT	CGCTGAGGCG	ACCCCCGGTG	ACAACGTCGG	CTTTAACGTG	900
	AAGAACGTTT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
5	CAAGAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
	TCCTGAACCA	CCCCGGACAG	ATTGGAAACG	GTTATGCGCC	CGTGCTGGAC	1050
	TGCCACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
	CGACCGTCGC	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
	CTGGCGACGC	CGCGATCGTG	CGCATGGTGC	CGCAGAAGCC	TATGTGCGTG	1200
10	GAGGTCTTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCEG	TGCGTGACAT	1250
	GCGCCAGACC	GTCGCTGTCT	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
	GTTCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

15

2) INFORMATION FOR SEQ ID NO: 865

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptosporidium parvum*

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

30

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
	GCAATTTCGAA	ACCCCAAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCTTTATTGG	TTGTCCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
35	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTGAGAC	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
	TTACAACACC	GAGAAGATCC	CATTCGTTGC	CATTTCTGGT	TTCGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
40	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCCATTAAC	AAGATGTTTA	CAAGATAGGT	GGTGTAGGTA	550
	CTGTCCCAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
	GTTACCTTCG	CTCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATTAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
45	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
	TATCGTCCTC	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
	TTGACTGTCA	CACCGCTCAC	ATTTCTTGCA	AATTCCAGAC	TATCACTGCT	900
	AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
50	CAAGTCTGGT	GATGCTGCTT	TGGTTGTTAT	GCAACCTTTG	AAGCCACTTT	1000
	GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
	GA					1052

55

2) INFORMATION FOR SEQ ID NO: 866

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 837 bases
- (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 35552

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGCGGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
15	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
20	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
25	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

30

2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zoogloea ramigera*

(B) STRAIN: ATCC 25935

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

	AAGGTATTTCG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
	ACAACAGCAG	CTGGGCGACG	GCATTGTCCG	TACCATTGCA	CTGGGTACCT	100
50	CCGACGGCCT	GCGTCGCGGC	ATGATGATCC	AGAACACCGG	CAAACCTATC	150
	ATGGTGCCAG	TCGGTAAAGC	AACCCTGGGT	CGCATCATGG	ACGTGCTGGG	200
	TAACCCGATC	GACGAATGCG	GCGCGGTGCG	TCACGACCAG	ATCGCTTCGA	250
	TCCACCGCGC	TCCTCCTGCG	TACGACGAAC	TGTCGCCATC	GCAAGATCTG	300
	CTGGAAACCG	GCATTAAAGT	TATTGACCTG	GTGTGCCCCG	TCGCCAAGGG	350
55	CGGTAAAGTC	GGTCTGTTCG	GCGGTGCAGG	TGTGGGCAAG	ACCGTGAACA	400
	TGATGGAACT	GATCAACAAC	ATCGCCAAAG	CACACTCGGG	TCTGTCCGTG	450
	TTTGCCGGTG	TGGGTGAGCG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	GATGGCTGAC	GCCAAAGTGG	TCGATCTGGA	AAATCCAGAG	AACTCCAAGG	550
	TTGCGATGGT	CTACGGTCAG	ATGAATGAAC	CACCAGGCAA	CCGTCTGCGC	600
60	GTGGCGCTGA	CCGGTCTGAC	CATGGCTGAA	GCATTCCGTG	ACGAAGGCAA	650

AGACGTTCTG	TTCTTCGTGG	ACAACATCTA	CCGCTTCAC	CTGGCCGGTA	700
CCGAAGTATC	GGCACTGCTG	GGCCGTATGC	CATCGGCTGT	GGGTTACCAG	750
CCTACGCTGG	CCGAAGAAAT	GGGTCGCCTG	CAAGAGCGCA	TCACTTCGAC	800
CAAGACCGGT	TCGATCAC				818

5

2) INFORMATION FOR SEQ ID NO: 868

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 43867

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

CTATCTTAGT	AGTATCTGCT	GCTGATGGCC	CAATGCCACA	AACTCGTGAA	50
25 CACATTCTTT	TATCACGTAA	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	100
AAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	150
TGGAAGTTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	200
CCTGTAAATCT	CTGGTTCTGC	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	250
TGAGCAAAAA	ATCTTAGACT	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	300
30 CACCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	400
TCAAATCAAA	GTCGGTGAAG	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	450
CAAGCAAAAC	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	500
TACGCTGAAG	CTGGTGACAA	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	550
35 TGATGACGTA	CAACGTGGTC	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	600
CACATACAAA	ATTCAAAGCG	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	650
GGTCGTCATA	CACCATTCTT	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	700
TACTACTGAC	GTAACCTGGT	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
40 TTATGCCTGG	CGATAACGTT	GAAATGGA			778

2) INFORMATION FOR SEQ ID NO: 869

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R689

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

TGGTCCTATG	CCTCAAACAC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
60 GTGTACCATA	CATCGTTGTT	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	100

488

	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCTGACT	TATTGTAGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGCGATGCT	TCATACGAAG	AAAAAATCAT	GGAATTAATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGACA	CTGACAAACC	300
5	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAATCGTTG	GTATTGCTGA	AGAAACTGCT	AAAACAACCTG	TAACCTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGTGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
10	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	600
	TTACGTTTTA	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

15 2) INFORMATION FOR SEQ ID NO: 870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

30	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
	GTACCATAACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	TCGTGACTTA	TTGTCAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCTGGTTC	TGCTTTGAAA	200
35	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AAACTGCTAA	AACAACCTGTA	ACTGGTGTTG	450
40	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTTAAC	AAAAGAAGAA	GGTGGACGTC	ACACACCAT	CTTC	644

45

2) INFORMATION FOR SEQ ID NO: 871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R758

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTT	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
5	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCTGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
10	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACTGTAA	CTGGTGTGTA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTA	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTAAAG	CTGAAGTTTA	600
15	CGTTTTAACA	AAAGAAGAAG	GTGGACGTCA	CACTCCA		637

2) INFORMATION FOR SEQ ID NO: 872

20

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 643 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

35	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
40	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AACTGCTAA	AACAACTGTA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
45	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	CTT	643

50

2) INFORMATION FOR SEQ ID NO: 873

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 641 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

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GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC      50
GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA      100
AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT      150
10 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA      200
GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC      250
TGCAGTTGAC GAATACGTTT CAACTCCAGA ACGTGATACT GACAAACCAT      300
TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA      400
15 AATCGTTGGT ATTGCTGACG AAACCTGCTAA AACAACTGTA ACAGGTGTTG      450
AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAAA GCTGAAGTTT      600
ATGTTTTGAC AAAAGAAGAA GGTGGACGTC ACACTCCATT C                641
20

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2) INFORMATION FOR SEQ ID NO: 874

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 35 (B) STRAIN: LSPQ 2514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

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ACCAGCATTG GTAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
40 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC      100
GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC      150
TTTAGAAGGC GATGCTCAAT ACGAAGAAA AATCTTAGAA TTAATGCAAG      200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTG      250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC      300
45 TACAGGCCGT GTTGAACGTG GCAAATCAA AGTTGGTGAA GAAGTTGAAA      350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG      400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT      450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG      500
CTCCAGGTTT AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT      550
50 TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG      600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC      650
CAGAAGGTAC TGAAATGGTT ATGCCTGGCG A                681

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55

2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: R591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

	ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTC	TTAAACAAAG	50
	TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
	CGTGACTTAT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
15	CGCTGGTTCT	GCATTAAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
	AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
	CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
	CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
	AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
20	ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
	TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
	AACGTGGTCA	AGTATTAGCT	GCTCCTGGTT	CTATTACACC	ACACACAAAA	550
	TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
	TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCCGT	ACTACTGACG	650
25	TAAGTGGTGT	TGTAACTTA	CCAGA			675

2) INFORMATION FOR SEQ ID NO: 876

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

45	TCTTATTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTTGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
	TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200
	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACCTCC	250
50	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTTCG	ACGTGAAGAC	500
55	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCAC	AATTCTATTT	CCGTACTACT	650
	GACGTAACTG	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
60	TGGC					704

2) INFORMATION FOR SEQ ID NO: 877

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 15 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

20	TCTTAGTTGT ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC	50
	ATCTTATTAT CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA	100
	CAAAGTTGAC ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG	150
	AAGTTCGTGA CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT	200
	GTAATCGCTG GTTCTGCATT AAAAGCATTA GAAGGCGATG CTGAATACGA	250
	ACAAAAAATC TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAATC	300
25	CAGAACGTGA TTCTGACAAA CCATTCATGA TGCCAGTTGA GGACGTATTC	350
	TCAATCACTG GTCGTGGTAC TGTTGCTACA GGCCGTGTTG AACGTGGTCA	400
	AATCAAAGTT GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA	450
	AAACAACCTG TACTGGTGTG GAAATGTTCC GTAAATTATT AGACTACGCT	500
	GAAGCTGGTG ACAACATCGG TGCTTTATTA CGTGGTGTG CACGTGAAGA	550
30	CGTACAACGT GGTCAAGTAT TAGCTGCTCC TGGTTCCTATT ACACCACACA	600
	CAAAATTCAA AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT	650
	CACACTCCAT TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC	700
	TGACGTAAC TGGTGTGTAA ACTTACCAGA AGGTACAGAA ATGGTTATGC	750
35	CTGGCGACAA CGTTGAAATG	770

2) INFORMATION FOR SEQ ID NO: 878

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 50 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

55	TTGTATTCTT AAACAAAGTT GACATGGTAG ACGACGAAGA ATTATTAGAA	50
	TTAGTTGAAA TGGAAGTTCG TGACTTATTA AGCGAATATG ACTTCCCAGG	100
	TGACGATGTA CCTGTAATCG CTGGTTCCTGC ATTAAGAGCA TTAGAAGGCG	150
	ATGCTGAATA CGAACAAAAA ATCTTAGACT TAATGCAAGC AGTTGATGAT	200
	TACATTCCAA CTCCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT	250
	TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT ACAGGCCGTG	300
60	TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT CATCGGTATG	350

	CACGAAACTT	CTAAAACAAC	TGTTACTGGT	GTAGAAATGT	TCCGTAAATT	400
	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	CGGTGCTTTA	TTACGTGGTG	450
	TTGCACGTGA	AGACGTACAA	CGTGGTCAAG	TATTAGCTGC	TCCTGGTTCT	500
	ATTACACCAC	ACACAAAATT	CAAAGCTGAA	GTATACGTAT	TATCTAAAGA	550
5	TGAAGGTGGA	CGTCACACTC	CATTCTTCAC	TAACTATCGC	CCACAATTCT	600
	ATTTCCGTAC	TACTGACGTA	ACTGGTGTTG	TAAACTTACC	AGAAGGTACA	650
	GAAATGGTTA	TGCCTGGCGA	CAACGTTGAA	ATGACAGTTG	AATTAATCGC	700
	TCCAATCGCT	ATCGAA				716

10

2) INFORMATION FOR SEQ ID NO: 879

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R764

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
30	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACC	TATTGTCTGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTCTGT	AATCGCCGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
35	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
	TGAAATGTTC	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
40	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

2) INFORMATION FOR SEQ ID NO: 880

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

60	CGGCGCGATC	CTGGTTTGCT	CGGCTGCCGA	CGGCCCATG	CCGCAGACCC	50
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	GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCCTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAAGTGGT	150
	CGAGATGGAA	GTTGCGGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
	AACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
5	GACAACGGCA	TCGGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
	CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCCTGATGC	350
	CGATCGAAGA	CGTGTTCCTG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
	CGTGTAAGAG	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCGG	450
	CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
10	AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
	GGCACCAAGC	GTGAAGACGT	AGAGCGTGCC	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTAC	GTGCTGTCCA	650
	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
15	CGTAGAGATG	GTAATGCCCG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
	TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

20 2) INFORMATION FOR SEQ ID NO: 881

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

35	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATAACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
40	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTG	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
45	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

50

2) INFORMATION FOR SEQ ID NO: 882

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

495

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATAACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
10	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
15	TACAGGCCGT	GTTGAACGTG	GACAAGTTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTTGAA	450
	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
20	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAT	ACACCA		636

2) INFORMATION FOR SEQ ID NO: 883

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

40	GGTCCTATGC	CTCAAACACG	TGAACATATC	TTATTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTAT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTATT	AGAATTAGTA	GAAATGGAAG	TCGTGACTT	ATTATCAGAA	150
	TACGATTTCC	CAGGCGATGA	TGTTCCAGTT	ATCGCAGGTT	CTGCTTTGAA	200
	AGCTTTTAGAA	GGCGACGAGT	CTTATGAAGA	AAAAATCTTA	GAATTAATGG	250
45	CTGCAGTTGA	CGAATATATC	CCAACCTCCAG	AACGTGATAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGTGAAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTAAAGAC	GAAACATCTA	AAACAACCTGT	TACAGGTGTT	450
	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
50	TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
	TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAAATTCAA	AGCTGAAGTA	600
	TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

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2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
TTTCCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
TATTACGTGG	TGTTGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCATTCTTC		640

2) INFORMATION FOR SEQ ID NO: 885

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

TGCCTCAAAC	TCGTGAACAC	ATCCTATTGT	CTCGTCAAGT	TGGTGTTCCT	50
TACATCGTTG	TATTCTTGAA	CAAAGTAGAT	ATGGTTGATG	ACGAAGAATT	100
ACTAGAATTA	GTTGAAATGG	AAGTTCGTGA	CCTATTAACA	GAATACGAAT	150
TCCCTGGTGA	CGATGTTTCT	GTAGTTGCTG	GATCAGCTTT	GAAAGCTCTA	200
GAAGGCGACG	CTTCATACGA	AGAAAAAATT	CTTGAATTAA	TGGCTGCAGT	250
TGACGAATAC	ATCCCAACTC	CAGAACGTGA	CAACGACAAA	CCATTTCATGA	300
TGCCAGTTGA	AGACGTGTTC	TCAATTACTG	GACGTGGTAC	TGTTGCTACA	350
GGTCGTGTTG	AACGTGGACA	AGTTCGCGTT	GGTGACGAAG	TTGAAGTTGT	400
TGGTATTGCT	GAAGAACTT	CAAAAACAAC	AGTTACTGGT	GTTGAAATGT	450
TCCGTAAATT	GTTAGACTAC	GCTGAAGCTG	GAGACAACAT	TGGTGCTTTA	500
CTACGTGGTG	TTGCACGTGA	AGACATCCAA	CGTGGACAAG	TTTTAGCTAA	550
ACCAGGTACA	ATCACACCTC	ATACAAAATT	CTCTGCAGAA	GTATACGTGT	600
TGACAAAAGA	AGAAGGTGGA	CGTCATACTC	CA		632

2) INFORMATION FOR SEQ ID NO: 886

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

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15 CGGCCCAATG CCTCAAACCTC GTGAACACAT CCTATTGTCT CGTCAAGTTG      50
   GTGTTTCCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT GGTTGATGAC      100
   GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA      150
   ATACGAATTC CCTGGTGACG ATGTTCTGTG AGTTGCTGGA TCAGCTTTGA      200
20 AAGCTCTAGA AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG      250
   GCTGCAGTTG ACGAATACAT CCCAACTCCA GAACGTGACA ACGACAAACC      300
   ATTCATGATG CCAGTTGAAG ACGTGTTCTC AATTACTGGA CGTGGTACTG      350
   TTGCTACAGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG TGACGAAGTT      400
   GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT      450
25 TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCTGGA GACAACATTG      500
   GTGCTTTACT ACGTGGTGTG GCACGTGAAG ACATCCAACG TGGACAAGTT      550
   TTAGCTAAAC CAGGTACAAT CACACCTCAT ACAAATTCT CTGCAGAAGT      600
   ATACGTGTTG ACAAAGAAG AAGGTGGACG TCATACTCCA      640

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2) INFORMATION FOR SEQ ID NO: 887

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

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50 ATCCTGGTTT GCTCCGCAGC TGACGGCCCA ATGCCACAGA CCCGCGAGCA      50
   CATCCTGCTG GCCCGCCAAG TTGGCGTTCC ATACATCATC GTGTTCTCTGA      100
   ACAAGTGCGA CCTGGTTGAC GACGCAGAAC TGCTGGAAC TGGTCGAAATG      150
   GAAGTGCGTG AATTGCTGTC GAAATACGAG TTCCCAGGCG ACGACGTACC      200
   AATCATCAAG GGTTCGGCAC GTATGGCGCT GGAAGGCAAA GAAGGCGAGA      250
   TGGGCGTTGA CGCCATCATG CGTCTGGCCG ATGCACTGGA CAGCTACATC      300
   CCTACGCCAG AGCGCGCAGT CGATGGCGCC TTCCTGATGC CAGTGGAAGA      350
55 CGTGTTCTCG ATCTCGGGTC GCGGTACCGT TGTGACCGGT CGTATCGAGC      400
   GCGGCGTGAT CAAGGTCGGC GAAGAGATCG AAATCGTCGG CATTATCGAC      450
   ACCGTCAAAA CCACTTGAC CCGCGTGGAA ATGTTCCGCA AGCTGCTGGA      500
   CCAGGGTCAA GCCGGCGACA ACGTTGGTCT GCTGCTGCGC GGCACCAAGC      550
   GTGAAGACGT ACAGCGTGGT CAGGTTCTGG CCAAGCCAGC GTCGATCAAG      600
60 CCGCACAACC ACTTCACCGG CGAGATCTAC GTTCTGTCGA AAGATGAAGG      650

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CGGCCGTCAC	ACCCCGTTCT	TCAACAATA	TCGTCCACAG	TTCTACTTCC	- 700
GTACGACTGA	CGTGACCGGT	TCGATCGAAC	TGCCAGCAGA	CAAAGAAATG	750
GTCATGCCAG	GCGACAACGT	GTCGATCACC	GTCAAGCTGA	TCAACCCGAT	800
CGCGAT					806

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2) INFORMATION FOR SEQ ID NO: 888

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: R503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

25

TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
TTTCCCAGGC	GATGATGTTC	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
TAGAAGGCCA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCA		634

40

2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 493 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

55

TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
TTCGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTA CTCTGTA	150
GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATT CAGCTCG	200
AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTCG	GACAGATGAA	CGAGCCCCC	250

60

	GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
5	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

2) INFORMATION FOR SEQ ID NO: 890

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

25	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	TGTCTTCACT	100
	GGTGTCGGTG	AACGTACTCG	TGAGGGTAAC	GATTTGTACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTACAG	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCCTGCCCC	GTGCCCCGTG	CGCTCTTACT	250
30	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATTT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCGTATC	CCCTCTGCCG	TCGGTTACCA	GCCACCCCTT	400
	GCCGTCGACA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
35	TTCCATCACC	TCCGTC				466

2) INFORMATION FOR SEQ ID NO: 891

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

	AGGAGCTGAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
55	ACTGGTGTCTG	GTGAGCGTAC	CCGTGAGGGT	AACGATCTGT	ACCACGAAAT	100
	GCAGGAGACC	TCGGTCATTG	AGCTCGAGGG	CGAGTCTAAG	GTGGCCCTGG	150
	TCTTTGGTCA	GATGAACGAG	CCCCCGGGTG	CTCGTGCCCG	TGTCGCTCTT	200
	ACTGGTCTTA	CCGTCGCCGA	GTACTTCCGT	GACCAGGAGG	GTCAGGATGG	250
	TTAGTTCTCG	TCCACTCATG	CCGAAACATG	TGCGTGTTCC	GAGGCTAATC	300
60	AACGTGCCAG	TGCTGCTTTT	CATCGACAAC	ATTTTCCGAT	TCACACAGGC	350

CGGTTCCGAG	GTGTCTGCCC	TGCTGGGTCG	TATCCCCCTCT	GCCGTCGGTT	400
ACCAGCCCAC	CCTCGCCGTC	GACATGGGTG	GCATGCAGGA	GCGTATCACC	450
ACCACCAAGA	AGGGCTCTAT	CACCTCCG			478

5

2) INFORMATION FOR SEQ ID NO: 892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 481 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 58950

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
TACGACAACT	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
25 TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
GTACCACGAA	ATGCAGGAAA	CTGGTGTCAT	TCAGCTCGAG	GGTGAATCCA	200
AGGTCGCCCT	CGTGTTCCGT	CAGATGAACG	AGCCCCCCGG	TGCCCGTGCC	250
CGTGTCGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
30 CCGGTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GTATCCCCTC	TGCCGTCGGT	400
TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

35

2) INFORMATION FOR SEQ ID NO: 893

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1208 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 14285

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
55 GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCGT	GGTGGTAAGA	250
TTGGTCTGTT	TGGCGGTGCC	GGTGTGGCA	AGACCGTGTT	CATCCAGGAG	300
CTCATCAACA	ACATCGCCAA	GGCCCACGGT	GGTTACTCCG	TCTTCACCGG	350
TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
60 AGACCTCTGT	CATTCAGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTT	450

501

	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCGTGTCG	CCTTGACCGG	500
	TTTGACTGTC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCCTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
5	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGCTGACG	800
	ATCTGACGGA	TCCCGCCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCGA	900
10	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCTTGAGCC	1100
	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
15	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

20 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

35	TTCAGGA	ACT	TATTGTA	AAGC	CGCCCTC	TTT	ATGCATT	GAG	GGTGA	AATAAG	50
	AAGGCTG	ACA	GGTAAT	AGAA	CAACATT	GGCC	AAGGCTC	ACG	GTGGTT	ACTC	100
	CGTGTT	CACT	GGTGTC	GGTG	AGCGT	ACCCG	TGAAGG	AAAC	GATCTG	TACC	150
	ATGAAAT	GCA	GGAAAC	CCCGC	GTCAT	CCAGC	TTGATG	GGCGA	GTCTA	AGGTC	200
40	GCCCTT	GTGT	TCGGTC	CAGAT	GAACG	AGCCC	CCTGG	AGCCC	GTGCCC	GTGT	250
	CGCTCT	TACT	GGTCTT	ACCG	TTGCC	GAATA	CTTCC	GTGAC	GAGGAG	GGGCC	300
	AAGATG	GTAC	GCCTTT	TTTAC	TCTTCT	TATT	CTTCG	GGTCG	GACTAC	AGAA	350
	CTAAC	CTGCT	CCAGT	GCTTC	TCTTC	ATTGA	TAACAT	TTTTC	CGTTTC	CACAC	400
	AAGCC	GGTTC	TGAGG	TGCT	GCCTT	GCTTG	GACGT	ATTCC	CTCTG	CCGTC	450
45	GGTTAC	CAGC	CCACT	CTCGC	CGTCG	ACATG	GGTGG	TATGC	AGGAAC	CGTAT	500
	CACAAC	CACC	AACAAG	GGGT	CCATT	ACTTC	CGTG				534

50 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

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5  CAAGGCTCAC GGTGGTTACT CCGTCTTCAC TGGTGTCTGGT GAGCGTACCC      50
   GTGAGGGTAA CGATCTGTAC CACGAAATGC AGGAGACCTC GGTCATTTCAG      100
   CTCGAGGGCG AGTCTAAGGT GGCCCTGGTC TTTGGTCAGA TGAACGAGCC      150
   CCCGGGTGCT CGTGCCCGTG TCGCTCTTAC TGGTCTTACC GTCGCCGAGT      200
10  ACTTCCGTGA CCAGGAGGGT CAGGATGGTT AGTTCTCGTC CACTCATGCC      250
   GAAACATGTG CGTGTTCGGA GGCTAATCAA CGTGCCAGTG CTGCTTTTCA      300
   TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCCGAGGT GTCTGCCCTG      350
   CTGGGTCGTA TCCCCTCTGC CGTCGGTTAC CAGCCCACCC TCGCCGTCGA      400
   CATGGGTGGC ATGCAGGAGC GTATCACCAC CACCAAGAAG GGCTCTAT      448
15

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2) INFORMATION FOR SEQ ID NO: 896

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*
 30 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

```

   ATTCAGGAGC TGATTGTAAG TTGCCAATCC ATGAACTGGA GATTTGGTGT      50
35  GACCCATAGA ACTAACAAAT TATTTAGAAC AACATCGCCA AGGCTCACGG      100
   TGGTTACTCC GTCTTCTGTG GTGTCGGTGA GCGTACTCGT GAGGGTAACG      150
   ATCTGTACCA CGAAATGCAG GAGACTGGTG TCATCCAGCT CGAGGGTGAC      200
   TCCAAGGTCG CTCTGGTCTT CGGTCAGATG AACGAGCCCC CGGGTGCCCCG      250
   TGCCCGTGTC GCCCTTACCG GTCTGACCAT TGCCGAGTAC TTCCGTGACG      300
40  AGGAGGGTCA GGACGTGCTG CTCTTCATTG ACAACATTTT CCGTTTCACC      350
   CAGGCCGGTT CTGAGGTGTC TGCCCTTCTG GGTCGTATCC CCTCTGCCGT      400
   CGGTTACCAG CCCACTCTGG CCGTCGACAT GGGTGGTATG CAGGAGCGTA      450
   TTACCACCAC CACCAAGGGT TCCATTACCT CCG                          483
45

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2) INFORMATION FOR SEQ ID NO: 897

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 60 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAGTACC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCTCTG	TCCGTCCCTY	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
 (D) STRAIN: WSA-214

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

45	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCTCTGG	TACTGGTGAA	TTCGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTTACC	CTCGGTGTCC	250
50	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCTTTC	GTTCTTATCT	CCGGTTTCAA	450
	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCTGCG	TACAAGGGTT	500
55	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
60	GTTGTACCTT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800

	TGTGCTAACT	TGACACTCAG	CGCTCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCGTGGT	950
	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
5	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTCTGTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTC	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCCTT	1200
	CCAAGCCCAT	GTGTGTTGAG	GCTTTCACCG	AGTACCCTCC	TCTCGGTCGT	1250
10	TTCGCCGTTT	GCGAGTAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACG	GGA				1363

15

2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1147 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
- (B) STRAIN: ATCC 24292

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
35	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCTGAGGCCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
40	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAACTGCCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCAA	GCGTCCTTCC	GACAAGCCCC	600
	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCGGTGGTAT	CGGAACTGTT	650
45	CCTGTCGGCC	GTATCGAGAC	TGGTGTCCTC	AAGCCCGGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
	CAAGAACGAC	CCCGCTCTGG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
50	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
55	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

2) INFORMATION FOR SEQ ID NO: 900

60

(i) SEQUENCE CHARACTERISTICS:

505

- (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
15	GTTTCGAGACT	CCCAAGTACT	ATGTCACCGT	CATTGGTACG	TCGACTCGCG	100
	CGAGACTGGT	CGCAATTTCC	ACGTCGCTAA	CGTGCTTGAA	CAGACGCTCC	150
	CGGCCACCGT	GACTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCTG	200
	ACTGCGCTAT	CCTCATTATC	GCTGCCGGCA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	300
20	CGGTGTTAAG	CAGCTCATCG	TCGCTATCAA	CAAGATGGAC	ACCACCAAGT	350
	GGTCTGAGGC	CCGTTTCCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGACCGTC	GCTTTCGTCC	CCATCTCTGG	450
	TTTCCACGGC	GACAACATGC	TTTCCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGCTGGGA	GAAGGAGACC	AAGGCTGGCA	AGTCCACCGG	CAAGACCCTC	550
25	CTTGAGGCCA	TCGACTCCAT	CGAGCCCCCC	AAGCGCCCCA	GCGACAAGCC	600
	CCTCCGCCTT	CCCCTTCAGG	ATGTGTACAA	GATCGGCGGT	ATCGGCACAG	650
	TCCCTGTCTG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCCG	CATGGTCGTG	700
	ACCTTCGCTC	CTTCCAACGT	CACCACCGAA	GTCAAGTCCG	TTGAGATGCA	750
	CCACGAGCAG	CTCTCCGAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
30	TCAAGAACGT	CTCCGTCAAG	GAGATCCGTC	GTGGCAACGT	CGCCGGTGAC	850
	TCCAAGAACG	ACCCCCCTCT	GGGTCCCGCT	TCTTTCGATG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGGTCGGTGC	TGGCTACGCC	CCCGTCCTCG	950
	ACTGCCACAC	CGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CAAGGAGAAG	1000
	ATCGACCGCC	GTACCGGCAA	GTCTGTCTGAG	TCCGCCCCCA	AGTTCATCAA	1050
35	GTCTGGCGAC	TCTGCCATCG	TCAAGATGAT	TCCCTCCAAG	CCCATGTGCG	1100
	TTGAGGCTTT	CACCGACTAC	CCTCCTCTGG	GCCGCTTCGC	CGTCCGTGAC	1150

40 2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

55	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTCTTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
60	GCAAGACCTT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250

	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
5	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCCTCAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACC GGAA	AGTCTGTTGA	GAACAACCCC	700
10	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

15 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

30	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTCATCGC	GATTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
35	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
40	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCTCCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTGCG	CCGTATCGAG	600
	ACTGGTGTCC	TGAAGCCCGG	CATGGTCTGC	ACCTTTGCCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
45	GTGTTCCCGG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTCGGCAA	CGGCTACGCC	CCGGTTCTGG	ACTGCCACAC	CGCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
50	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000
	TCAAGCTGAC	GCCCTCGAAG	CCCATGTGCG	TTGAGGCCTT	CACTGACTAC	1050
	CCCCCT					1056

55

2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1366 bases
 60 (B) TYPE: Nucleic acid

507

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

CAAGGCTGAG	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	50
TCCAGACTGC	CAAGTACGAG	GTTACCGTCA	TTGACGCCCC	CGGTCACCGT	100
GATTTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCCG	ATTGCGCTAT	150
15 TCTCATCATT	GCCTCTGGTA	CTGGTGAATT	CGAGGCTGGT	ATCTCCAAGG	200
ATGGCCAGAC	TCGTGAGCAC	GCTCTTTTGG	CTTTCACCCT	CGGTGTCCGT	250
CAGCTCATTG	TTGCCCTCAA	CAAGATGGAC	ACTTGCAAGT	GGTCTCAGGG	300
TGAGTACTCG	TACCTGCGTT	TGGCCTTGAA	TATCTTACTA	ATGCACCATA	350
GATCGTTACA	ACGAAATTGT	CAAGGAGACT	TCCAACCTCA	TCAAGAAGGT	400
20 CGGATACAAC	CCTAAGAACG	TTCCTTTTCGT	TCCTATCTCC	GGTTTCAACG	450
GTGACAACAT	GCTTGAGCCC	TCCCCCAACT	GCCCCTGGTA	CAAGGGTTGG	500
GAGAAGGAGA	CCAAGGCCGG	TAAGGTCACT	GGTAAGACCC	TCCTCGAGGC	550
CATCGACGCC	ATTGAGCCCC	CTACCCGTCC	CGCCAACAAG	GTTAGTCCCT	600
CCTCGACTAC	TCAAACCCTC	CTCATAAGTT	CAGATTACTG	ACTCGTTCAC	650
25 AGCCCCCTCCG	TCTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATTGGA	700
ACGGTTCCCCG	TCGGTCGTGT	TGAGACTGGT	ACCATCGTTC	CTGGTATGGT	750
TGTCACCTTG	TAAGTCACTC	TCCTCGCTTA	TCCTACCTGA	AATCATCATG	800
TGCTAACTTG	ACACTCAGCG	CTCCCGCAA	CGTCACCACT	GAAGTCAAGA	850
GTGTTGAAAT	GCACCACCAG	CAGCTCACTG	CCGGTCAGCC	CGGTGACAAC	900
30 GTTGGTTTCA	ACGTGAAGAA	CGTCTCCGTC	AAGGAAATCC	GTCTGGGTAA	950
CGTTGCTGGT	GACAGCAAGA	ACGACCCCCC	TGCCGGTGCT	GCCTCCTTCA	1000
ACGCCCAGGT	CATCGTCCTC	AACCACCCCC	GTCAGGTCGG	TGCTGGTTAC	1050
GCCCCAGTCC	TCGATTGCCA	CACTGCCCCA	ATTGCTTGCA	AGTTCGCTGA	1100
GCTCCTCGAG	AAGATTGACC	GTCGTACCGG	AAAGTCTGTT	GAGGACCACC	1150
35 CCAAGTTCAT	CAAGTCCGGT	GACGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1200
AAGCCCATGT	GTGTTGAGGC	TTTCACCGAG	TACCTCCTC	TCGGTCGTTT	1250
CGCCGTTTCG	GAGTAAGTTT	TATCTCCGTT	GTCTATTTTC	CATCCTTCCC	1300
TTCTCCTCCG	TCTTCCATAT	ATATTTTTTC	AGTTATATGT	GACTAACCAC	1350
40 AAATCACGGG	AATAGC				1366

2) INFORMATION FOR SEQ ID NO: 904

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*
(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

CTATTATCGT	TGTTGCCGCT	TCCGACGGTC	AAATGCCCCA	GACTCGTGAG	50
60 CATCTGCTGC	TCGCCCCGCA	GGTCGGTGTC	CAGAAGATCG	TTGTCTTCGT	100

	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTG	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
5	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTGCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCGA	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
10	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAAGTTC	CTTGCTCTCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCACT	GCCGACGAGT	CGTGTGCCCT	GTACTGGCCA	GAAGGCACCG	750
	AGGACGCCCA	TGACAAGCTT	GTTATGCCCG	GTGACAACGT	CGAGATGGTT	800
15	TGCGAGCTCC	ATGCACCACA	CGTCTTGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Aspergillus niger*
- (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

35	CGGTGCTATC	ATTGTCGTCG	CCGCCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
40	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	GCGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTTCTCCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCTCCGGCC	GTGTCGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
45	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCCG	CCGTGAGGAT	CTCCGCCGTG	GTATGGTCAT	650
	TGCCGCTCCT	GGCAGCGCCA	AGGCCAACAG	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
50	TACCGTCCCC	AGCTGTTCAT	CCGCACTGCC	GGTAAAGTAA	ATTGCATTCT	800
	ATTCCGCTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
	GCTGAGTTCA	GCTTCCCCGA	CGGAGACCA	TCCCGCCGTA	TCATGCCCGG	900
	TGACAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
55	CCGGTCAGCG	CTTCAAC				967

2) INFORMATION FOR SEQ ID NO: 906

60

(i) SEQUENCE CHARACTERISTICS:

509

- (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

15	TGGTGCTATT	ATTGTTGTTG	CCGCTTCCGA	CGGTCAAATG	CCCCAGACTC	50
	GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTCAGAA	GATCGTTGTC	100
	TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
	CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
	AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
	CCCACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
20	TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
	TCGAGGATGT	CTTCTCCATT	GCTGGTCGTG	GTACCGTCGT	CTCTGGCCGT	400
	GTCGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
	GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
	AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
25	GGTGTTAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
	ACAGGTTAAG	GCGCACAAGA	AGTTCCTTGT	CTCCATGTAT	GTGCTGAGCA	650
	AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAACTA	CAGGCCGCAA	700
	ATGTTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
	CACCGAGGAT	GCCCACGACA	AGCTTGTCAT	GCCC GG TGAC	AACGTCGAGA	800
30	TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
	AA					852

35 2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

50

55	GGTGCTATTG	TTGTCGTTGC	TGCTTCGGAT	GGTCATGATG	TATGGACAGG	50
	CCCTTTGCTA	CTGAATGGTT	TCAAGATCTC	GCGCTTACAC	GTATTATAAT	100
	AGGCCCCAGA	CCCGGGAGCA	CTTGCTGCTT	GCCCGTCAGG	TCGGTGTCCA	150
	GAAGATCGTC	GTTTTTGTCA	ACAAGATTGA	TGCCGTTGAG	GACCTTGAGA	200
55	TGTTGGAGCT	TGTCGAGTTG	GAAATGCGCG	AGCTCCTTAG	CAGCTACGGC	250
	TTCGAGGGCG	AAGAGACTCC	CATCATCTTC	GGTTCGTGCTC	TGTGTGCTTT	300
	GGAGGACCGT	CGCCCCGACA	TTGGTGCCGA	GCGTATCGAC	GAGCTCATGA	350
	AGGCCGTTGA	CACCTGGATC	CCTACCCCTC	AGCGTGATCT	TGACAAGCCT	400
	TTCCTCATGT	CTGTGAGGGA	AGTCTTCTCC	ATCGCCGGTC	GTGGTACCGT	450
60	TGCCTCCGGC	CGTGTCGAAC	GTGGTATCCT	GAAGAAGGAC	AGCGAAGTCG	500

510

	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
5	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTTCG	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
10	CTGGCCAGCG	CTTCAA				966

2) INFORMATION FOR SEQ ID NO: 908

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
- (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

30	GGTGCTATCA	TCGTCGTTGC	TGCTTCCGAT	GGTCAGATGC	CCCAGACCCG	50
	TGAGCACTTG	CTGCTCGCCC	GTCAGGTCGG	TGTTTCAGAAG	ATCGTTGTCT	100
	TCGTCAACAA	GGTCGATGCT	GTCGAAGACC	CGGAGATGTT	GGAATCGTC	150
	GAGATGGAGA	TGCGTGAGTT	ACTCACCAGC	TACGGCTTCG	AGGGCGACGA	200
	GACACCCATC	ATCATGGGTT	CCGCTCTATG	CGCCATCGAG	GGCCGCCAGC	250
35	CCGAGATCGG	TGTTACCAAG	GTCGACGAGC	TAATGGACGC	TGTCGACTCA	300
	TGGATCCCCA	CCCCTCAGCG	TGAGACCGAG	AAGCCTTTCC	TCATGGCTGT	350
	TGAGGATGTC	TTCTCGATTG	CTGGACGTGG	TACCGTCGTT	TCGGGCCGTG	400
	TCGAGCGCGG	TATCTTGAAG	CGTGACGCTG	AAGTCGAGCT	TGTCGGCAAG	450
	GGCACCGCGC	CAATCAAGAC	CAAGGTCACT	GATATTGAGA	CCTTCAAGAA	500
40	GTCGTGCGAG	GAGTCGCGCG	CGGGTGATAA	CTCCGGTCTT	CTCCTCCGTG	550
	GTGTCAAGCG	TGATGACGTT	CGCCGCGGTA	TGGTTGTTTC	CGTTCCCGGA	600
	CAAGTCAAGG	CTCACAAGAA	GTTCCTTGTC	TCCATGTACG	TTCTAAGCAA	650
	AGAGGAGGGT	GGTCGTCACA	CCGGCTTCGG	CGAGAACTAC	AGGCCGCAA	700
	TGTTTCATCCG	AACTGCCGAT	GAATCCTGCG	CACTTCACTT	CCCAGAGGGT	750
45	ACCGAGGATG	CGCACGACAA	GCTAGTTATG	CCCGGTGACA	ACGTCGAGAT	800
	GGTCTGCGAA	CTCCACCAGC	CCCACGTTCT	AGAGACCGGT	CAGCG	845

2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

```

5   CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG      50
    AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG      100
    CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT      150
    CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTGCAAT      200
10  TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC      250
    CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA      300
    GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA      350
    TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG      400
    GAAGTTTCTT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA      450
15  GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA      500
    AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT      550
    TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT      600
    CAAGCGTGAG GACATTTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA      650
    CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT      700
20  GAAGGTGGTC GTCGTA CTGG ATTTCGGCGCC AACTACCGTC CTCAAGCTTT      750
    CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT      800
    GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT      850
    CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC      900
    ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G              931
25
  
```

2) INFORMATION FOR SEQ ID NO: 910

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

```

45  CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG      50
    AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG      100
    CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT      150
    CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTGCAAT      200
    TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC      250
    CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA      300
50  GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA      350
    TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG      400
    GAAGTTTCTT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA      450
    GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA      500
    AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT      550
55  TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT      600
    CAAGCGTGAG GACATTTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA      650
    CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT      700
    GAAGGTGGTC GTCGTA CTGG ATTTCGGCGCC AACTACCGTC CTCAAGCTTT      750
    CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT      800
60  GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT      850
  
```

CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

5

2) INFORMATION FOR SEQ ID NO: 911

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

20

2) INFORMATION FOR SEQ ID NO: 912

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

35

2) INFORMATION FOR SEQ ID NO: 913

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

GACGGYSYCA TGCKCAGAC

20

50

2) INFORMATION FOR SEQ ID NO: 914

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

60

513

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

GAARAGCTGC GGRCGRTAGT G

21

2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

2) INFORMATION FOR SEQ ID NO: 918

(i) SEQUENCE CHARACTERISTICS:

514

(A) LENGTH: 1391 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
 (E) ACCESSION NUMBER: J01672

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCGCGGTG	50
15	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
20	ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGA AACCAT	CTCTACCGGT	TCGCTTTCAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
25	GCACGTAAAC	TGGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
30	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAATTGG	TGTGATGTTC	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTTCGTCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGG TAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
35	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGA ACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTTTAA	1300
40	TCGTCTTGTT	TGATACACAA	GGGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

45 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCGART CITMIGGIAA RAC

23

60

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

TARAAYTTIA RIGCIYKICC ICC

23

2) INFORMATION FOR SEQ ID NO: 923

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

GACGCIGCCA TCCTGATGAT C

21

5 2) INFORMATION FOR SEQ ID NO: 924

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

10 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

20

2) INFORMATION FOR SEQ ID NO: 925

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

25 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

35

2) INFORMATION FOR SEQ ID NO: 926

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

50

2) INFORMATION FOR SEQ ID NO: 927

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

5 ACGCGGAGAA GGTGCGCTT

19

2) INFORMATION FOR SEQ ID NO: 928

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

20

GGTCGTTCTT CGAGTCACCG CA

22

25 2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*

(B) STRAIN: ATCC 25285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

40

TTCAGCATGC	CATTTCAAAA	CAGGCCGAAG	CCGATATCGT	GATTATCGCT	50
GCTTGTGGGG	AGCGTGCAA	TGAAGTTGTG	GAAATCTTTA	CCGAATTTCC	100
GGAATTGGTG	GACCCGCACA	CGGGACGTAA	GCTGATGGAG	CGTACCATTA	150
TTATCGCAAA	TACATCGAAC	ATGCCGGTAG	CAGCGCGTGA	AGCTTCTGTG	200
45 TATACGGCCA	TGACGATTGC	CGAATACTAT	CGTGCCATGG	GATTGAAAGT	250
CCTGCTGATG	GCAGACTCCA	CTTCCCCTTG	GGCGCAGGCA	TTGCGTGAGA	300
TGTCGAACCG	TATGGAGGAG	TTGCCCGGAC	CGGATGCATT	CCCGATGGAC	350
CTGTCCTCAA	TCATTTCTAA	CTTCTATGGC	CGTGCAGGCT	ACGTGAAACT	400
50 GAATAACGGC	GAGAGCGGTT	CTATTACCTT	TATCGGTACA	GTATCACC	448

2) INFORMATION FOR SEQ ID NO: 930

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides distasonis*

(B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

	GCTATCTCTA	AACAAGCGGA	AGCGGATATC	GTGATTATCG	CCGCCTGCGG	50
10	TGAGCGTGCG	AATGAGGTCG	TAGAGGTATT	TACGGAGTTC	CCGGAATTGG	100
	TAGACCCGCA	TACGGGACGT	AAATTGATGG	AACGTACGAT	CATTATCGCC	150
	AATACATCCA	ACATGCCGGT	AGCCGCTCGT	GAGGCATCCG	TATATACGGC	200
	GATGACCATC	GCCGAGTATT	ATCGCAGCAT	GGGTTTGAAG	GTTCTGTTGA	250
	TGGCCGACTC	TACTTCCCGC	TGGGCACAGG	CTTTGCGTGA	GATGTCCAAC	300
15	CGTTTGGAGG	AGTTGCCGGG	ACCGGATGCT	TTCCCGATGG	ACTTGTCCGC	350
	TATCGTGGCG	AACTTCTACG	CTCGTGCGGG	ATTCGTTTCAT	TTGAATAACA	400
	ACGCTACAGG	CTCCGTCACT	TTCATCGGTA	CGGTATCG		438

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas asaccharolytica*

(B) STRAIN: ATCC 25260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

	CCTCCAGCAC	GCTATCTCTA	AGCAGGCGGA	GGCTGATATC	GTCATTATGG	50
	CAGCCTGCGG	TGAGCGTGCT	AATGAGGTGG	TGGAGATCTT	TGCCGAGTTC	100
	CCTGAGCTCG	AAGACCCACA	CACGGGACGC	AAGCTGATGG	AGCGTACGAT	150
40	CATCATCGCT	AACACGAGTA	ACATGCCAGT	GGCTGCTCGT	GAGGCTTCCG	200
	TCTACACCGC	TATGACCATC	GCTGAGTACT	ACCGCTCGAT	GGGTCTCAAA	250
	GTA CTCTAA	TGGCTGACTC	GACCTCTCGC	TGGGCACAGG	CACTGCGTGA	300
	GATGTCTAAC	CGTCTAGAGG	AGCTGCCTGG	ACCAGATGCA	TTCCCGATGG	350
	ACTTGTCCGC	TATCGTGGCA	AACTTCTACG	CTCGTGCCGG	CTTCGTCTAT	400
45	CTCAACAACG	GTGAGACAGG	TTCTGTAACC	TTCATCGGTA	CGGTCTCTCC	450
	AGC					453

2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

5 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
 GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA 100
 TTCATGAACA AATGTGACAT GGTGACGAT GAAGAATTAC TAGAATTAGT 150
 10 TGAAATGGAA ATTCGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG 200
 ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT 250
 GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ATGTATTCTC AATCACTGGT CGTGAACAG TTGCAACTGG ACGTGTTGAA 400
 CGTGGACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA 450
 15 AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTC CGTAAATTAC 500
 TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGTT 550
 GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
 TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT 700
 20 TTCCGTACTA CTGACGTAAC TGGTATTGTT ACACTTCCAG AAGGTACTGA 750
 AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC 800
 CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC 835

25

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

40

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

55

2) INFORMATION FOR SEQ ID NO: 935

(i) SEQUENCE CHARACTERISTICS:

60

520

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

10 GGIAARWSIC ARYTITGYCA YAC

23

2) INFORMATION FOR SEQ ID NO: 936

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

25

TCISIIYTCIG GIARRCAIGG

20

2) INFORMATION FOR SEQ ID NO: 937

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

40

ATACIGARG YITTYGGIGA RTT

23

2) INFORMATION FOR SEQ ID NO: 938

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

55

CYIGTIGYIS WIGCRTGIGC

20

60

2) INFORMATION FOR SEQ ID NO: 939

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: D10023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

ATGTCTCAAG	TTCAAGAACA	ACATATATCA	GAGTCACAGC	TTCAGTACGG	50
GAACGGTTCG	TTGATGTCCA	CTGTACCAGC	AGACCTTTCA	CAGTCAGTCG	100
TTGATGGAAA	CGGCAACGGT	AGCAGCGAAG	ATATTGAGGC	CACCAACGGC	150
20 TCCGGCGATG	GTGGCGGATT	GCAGGAGCAA	GCGGAAGCGC	AAGGTGAAAT	200
GGAGGATGAA	GCATACGATG	AAGCTGCCTT	AGGTTTCGTTT	GTGCCAATAG	250
AAAAACTGCA	AGTGAACGGG	ATTACTATGG	CGGATGTGAA	AAAAC TAAGG	300
GAGAGTGGGC	TTCACACTGC	TGAAGCGGTA	GCATATGCTC	CCAGAAAGGA	350
TTTATTGGAA	ATCAAAGGTA	TATCGGAAGC	TAAGGCAGAT	AAGTTGCTAA	400
25 ACGAAGCGGC	AAGGCTAGTG	CCTATGGGAT	TTGTCACGGC	TGCTGATTTT	450
CATATGAGAA	GATCGGAGCT	GATTTGTTTG	ACAACGGGTT	CTAAGAATTT	500
GGACACTCTT	TTGGGTGGTG	GTGTGGAAAC	TGGTTCTATT	ACTGAGCTTT	550
TCGGTGAATT	CAGGACAGGT	AAGTCCCAGC	TATGTCACAC	TTTGGCCGTG	600
ACATGCCAAA	TTCCATTGGA	TATTGGTGCC	GGTGAAGGTA	AGTGT TTGTA	650
30 TATCGATACC	GAAGGTACTT	TCAGGCCGGT	AAGATTGGTA	TCCATAGCTC	700
AGCGGTTTCG	ATTAGACCCG	GATGATGCTT	TGAACAACGT	TGCGTATGCA	750
AGAGCCTATA	ACGCCGATCA	TCAGTTAAGA	CTTCTGGATG	CTGCTGCCCA	800
AATGATGAGC	GAGTCTCGGT	TTTCCTTGAT	TGTGGTCGAT	TCTGTTATGG	850
CTCTATAACG	TACGGATTTT	TCTGGTCGTG	GTGAACTAAG	CGCAAGGCAA	900
35 ATGCATTTAG	CCAAATTTAT	GCGTGCTTTG	CAAAGGCTGG	CCGACCAATT	950
TGGTGTGCA	GTCGTCGTTA	CTAACCAAGT	GGTCGCCCAA	GTTGATGGTG	1000
GTATGGCTTT	TAATCCAGAT	CCAAAGAAGC	CTATCGGTGG	TAATATTATG	1050
GCACATTCTT	CCACCACGCG	ATTAGGTTTC	AAAAAGGGTA	AGGGATGTCA	1100
AAGATTATGC	AAAGTTGTTG	ACTCACCTTG	CTTACCAGAG	GCTGAATGTG	1150
40 TGTTTCGCGAT	CTATGAAGAT	GGTGTGTTGGTG	ACCCAGAGA	AGAAGACGAG	1200
TAG					1203

2) INFORMATION FOR SEQ ID NO: 940

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: GRF88
 (C) ACCESSION NUMBER: M87549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA\	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
5	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGGC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TTAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
10	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAACTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
15	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAAACCT	CTGCTGTAGA	GGTTCCTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGAA	AAAATTAAAG	900
20	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGPTCTCATAC	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
25	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAAC TAAG	CGAAAGACAG	1400
30	CAAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
35	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

2) INFORMATION FOR SEQ ID NO: 941

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus humicola*
 (B) STRAIN: ATCC 38294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

	CGTCCTTATC	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCC	CACGGTGGTT	50
	TCTCCGTCTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGACCTG	100
	TACCACGAGA	TGCGTGAGAC	TGGTGTGATC	AACCTCGAGG	GCGACTCCAA	150
20	GGTCGCTCTC	GTCTTCGGCC	AGATGAACGA	GCCCCCGGA	GCCCGTGCCC	200
	GTGTGCGCCT	TACCGGCCTC	ACCATCGCCG	AGTACTTCCG	TGACGAGGAG	250
	GGTCAGGACG	TGCTTCTCTT	CATCGACAAC	ATTTTCCGTT	TCACCCAGGC	300
	CGGTTCCGAG	GTGTCTGCCC	TTCTCGGTCG	TATCCCCTCG	GCCGTCGGTT	350
	ACCAGCCCAC	CCTCGCTACC	GACATGGGTT	CCATGCAGGA	GCGTATCACC	400
25	ACCACCAAGA	AGGGTTTCGAT	TACCTCCGTC			430

2) INFORMATION FOR SEQ ID NO: 942

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

45	CGTGATACGAT	GCTCTTGAGG	TGCAAAATGG	TAATGAGCGT	CTGGTGCTGG	50
	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TGCGTACCAT	CGCAATGGGT	100
	TCCTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAAGACC	TCGAACACCC	150
	GATCGAAGTC	CCGGTAGGTA	AAGCGACTCT	GGGCCGTATC	ATGAACGTAC	200
	TGGGTGAACC	GGTCGACATG	AAAGGCGAGA	TCGGTGAAGA	AGAGCGTTGG	250
50	GCGATTCACC	GCGCAGCACC	TTCCTACGAA	GAGCTGTCAA	ACTCTCAGGA	300
	ACTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	CCGTTTCGCTA	350
	AGGGCGGTAA	AGTTGGTCTG	TTCGGTGGTG	CGGGTGTAGG	TAAAACCGTA	400
	AACATGATGG	AGCTCATTCG	TAACATCGCG	ATCGAGCACT	CCGGTTACTC	450
	TGTGTTTTCG	GGCGTAGGTG	AACGTACTCG	TGAGGGGAAC	GACTTCTACC	500
55	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	GGTGTATGGC	550
	CAGATGAACG	AGCCGCCGGG	AAACCGTCTG	CGCGTAGCTC	TGACCGGTCT	600
	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTT	CTGCTGTTTCG	650
	TTGACAAACAT	CTATCGTTAC	ACCCTGGCCG	GTACCGAAGT	ATCCGCACTG	700
	CTGGGCCGTA	TGCCTTCAGC	GGTAGGTTAT	CAGCCGACCC	TGGCGGAAGA	750
60	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAAACC	GGTT	794

2) INFORMATION FOR SEQ ID NO: 943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTACGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATTGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
25	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
30	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
35	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACTGGTTCTA	TCAC				814

2) INFORMATION FOR SEQ ID NO: 944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55	GTGTACGATG	CTCTTGAGGT	GCAAAATGGT	AATGAGCGTC	TGGTGCTGGA	50
	AGTTCAGCAG	CAGCTCGGCG	GCGGTATCGT	CGGTACCATC	GCAATGGGTT	100
	CCTCCGACGG	TCTGCGTCGC	GGTCTGGATG	TAAAAGACCT	CGAACACCCG	150
	ATCGAAGTCC	CGGTAGGTAA	AGCGACTCTG	GGCCGTATCA	TGAACGTACT	200
60	GGGTGAACCG	GTCGACATGA	AAGGCGAGAT	CGGTGAAGAA	GAGCGTTGGG	250

	CGATTCACCG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTGCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTCCAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTT	TGCTGTTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
	ACCGTTCTA	TC				812

50

2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

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GCGACGCTAT CCCGCATGTT TACGATGCCC TGAAATTGGA CGAGAACGGT      50
CTGACTCTGG AAGTTCAACA ACTTCTGGGT GACGGCGTTG TCCGTACTAT      100
TGCAATGGGT AGTTCAGACG GCCTGAAACG CGGCATGTCT GTAAGCAATA      150
10 CTGGTGCGCC AATCACTGTG CCGGTAGGTA AAGGTACTTT GGGTCGTATT      200
GTCGACGTAT TGGGTACGCC TGTGTAGTAA GCAGGTCCGA TCGATACCGA      250
CAAGAGCCGT GCCATTACAC AAACGTCTCC GAAATTTCGAC GAGTTGTCTG      300
CAACTACCGA ATTGTTGGAA ACCGGTATTA AAGTGATCGA CTTGCTGTGT      350
CCGTTTGCTA AAGGCGGTAA AGTAGGTCGT TTCGGTGGTG CCGGTGTAGG      400
15 CAAAACCGTG AACATGATGG AATTGATCAA CAACATCGCC AAAGCGCACA      450
GCGGTCTGTC CGTGTTTCGA GGTGTGGGCG AGCGTACCCG TGAAGGTAAC      500
GACTTCTACC ACGAGATGAA AGATTCCAAC GTATTGGATA AAGTGGCAAT      550
GGTTTACGGT CAGATGAACG AACCTCCGGG CAACCGTTTG CGCGTCGCAT      600
TGACCGGTTT GACCATGGCG GAATACTTCC GTGACGAAAA AGACGAAAAC      650
20 GGTAAAGGTC GCGACGTATT GTTCTTCGTT GACAACATCT ACCGTTACAC      700
TCTGGCCGGT ACCGAAGTAT CTGCACTGTT GGGCCGTATG CTTTCTGCAG      750
TGGGTTACCA ACCGACATTG GCTGAAGAAA TGGGTCTGTTT GCAAGAGCGT      800
ATTACCTCTA CCCAAACCGG TTCCATTACT TC                        832

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25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

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TCCGCGCGAT GCCATTCCGC ATGTTTACGA CGCCCTGAAA TTGGATGCAA      50
ACGGCCTGAC TTTGGAAGTA CAACAGCTTC TGGGCGACGG CGTGGTTTCGT      100
45 ACTATTGCAA TGGGTAGTTC GGACGGTCTG AAACGCGGCA TGACTGTAAAG      150
CAATACAGAT GCGCCGATTA CTGTGCCGGT AGGTAAAGGT ACTTTGGGAC      200
GTATTGTCGA TGTGTGGGT ACACCTGTTG ATGAAGCAGG TCCGATTGAT      250
ACCGACAAAC ACCGTGCTAT CCATCAGACA GCTCCGAAAT TCGATGAGTT      300
GTCTGCTACT ACCGAGCTGC TGGAAACAGG CATTAAAGTG ATTGACTTGC      350
50 TGTGTCCGTT TGCCAAAGGC GGTAAAGTAG GTCTGTTTCGG TGGTGCCGGT      400
GTAGGCAAAA CCGTCAACAT GATGGAATTG ATTAACAACA TCGCCAAAGC      450
GCATAGTGGT TTGTCCGTGT TCGCCGGTGT GGGGGAACGT ACCCGTGAAG      500
GTAACGACTT CTACCACGAG ATGAAAGATT CCAACGTATT GGACAAAGTG      550
GCGATGGTTT ACGGTCAGAT GAACGAACCT CCGGGTAACC GTCTGCGTGT      600
55 AGCCTTGACC GGTTCGACGA TGGCCGAATA CTTCCGTGAT GAAAAAGACG      650
AAAGCGGCAA AGGTCGCGAC GTATTGTTCT TCGTGGACAA CATTACCGT      700
TACACTCTGG CCGGTACAGA AGTATCCGCA TTGCTCGGTC GTATGCCTTC      750
AGCAGTAGGT TACCAACCGA CATTGGCTGA AGAAATGGGT CGTCTGCAAG      800
AGCGTATTAC CCTCTACTCA AACAGGCTCC ATTACTTCTA      840

```

60

2) INFORMATION FOR SEQ ID NO: 948

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

20	GCAGCTGGCG	ACAAGCTACC	TGAGATCAAT	AATGCACTTG	TAGTCTATAA	50
	AAATGACGAA	AAAAAATCAA	AAATCGTCCT	TGAAGTAGCT	CTTGAGCTTG	100
	GTGATGGAGT	GGTTCGGACC	ATCGCTATGG	AATCAACGGA	TGGGTTGACT	150
	CGTGGCATGG	AAGTGCTAGA	TACTGGCCGT	CCAATTTCTG	TGCCAGTCGG	200
	CAAAGAAACA	CTTGGTCGCG	TCTTTAACGT	TTTGGGAGAT	ACCATTGACT	250
	TGGATGCTCC	TTTTGCGGAT	GATGCAGAGC	GCCAGCCAAT	CCATAAGAAA	300
25	GCTCCAACCT	TTGATGAGTT	GTCTACTTCT	TCAGAGATCT	TAGAGACAGG	350
	TATCAAGGTT	ATCGACCTGT	TAGCCCCTTA	TCTGAAAGGT	GGTAAAGTTG	400
	GACTCTTCGG	TGGTGCCGGA	GTGGGTAAGA	CCGTCTTGAT	TCAAGAATTG	450
	ATCCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTCTGTAT	TTACTGGCGT	500
	TGGGGAACGT	ACCCGTGAAG	GGAATGACCT	TTATTGGGAA	ATGAAAGAGT	550
30	CTGGTGTTAT	CGAGAAAACA	GCCATGGTCT	TCGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCGC	GTATGCGGGT	TGCTTTGACT	GGTTTGACGA	TTGCAGAATA	650
	CTTCCGTGAT	GTGGAAGGTC	AAGATGTCTT	GCTCTTCATT	GACAACATCT	700
	TCCGTTTCAC	GCAGGCAGGT	TCTGAAGTTT	CTGCCCTTTT	GGGTCGGATG	750
	CCGTCAGCCG	TTGGTTACCA	ACCAACACTT	GCGACAGAAA	TGGGGCAATT	800
35	GCAAGAGCGT	ATCACATCGA	CTAAGAAGGG	TTCTGTAACC	TCT	843

2) INFORMATION FOR SEQ ID NO: 949

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GAGATGGTAT	GGTCCGTACT	ATCGCCATGG	AATCAACAGA	TGTTTGGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAATGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GATGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAAC	TTGATGA	ATTGTCT	TACCTCT	TCTGAA	AATCC	TTGAAAC	AGG	350
	GATTAAG	GTTATC	GACCTT	CCTTAA	AGGT	GGTAAG	GTTG		400
	GACTTTT	TCGG	TGGTG	CCGGA	GTTGGT	AAAA	CCGTCT	TAAAT	450
	ATTCACA	ACA	TTGCC	CAAGA	ACACGG	TGGT	ATTTCA	GTAT	500
5	TGGGGA	ACGT	ACTCG	TGAGG	GTAAT	GACCT	TTACTG	GGAA	550
	CAGGTG	TAT	CGAGAA	ACA	GCCAT	TGGTAT	TTGGT	CAGAT	600
	CCAGGAG	CAC	GTATG	CGTGT	TGCCCT	AACT	GGTTT	GACAA	650
	CTTCCG	TGAT	GTGGA	AAGGCC	AAGAC	GCTGCT	TCTCTT	TATC	700
	TCCGTTT	CAC	TCAGG	CTGGT	TCAGA	AGTAT	CTGCC	CTTTT	750
10	CCATCAG	CCG	TTGGT	TACCA	ACCAAC	ACTT	GCTAC	GGA	800
	GCAAGAG	CGT	ATTAC	ATCAA	CTAAAA	AAGGG	TTCTG	TAA	841
								T	

15 2) INFORMATION FOR SEQ ID NO: 950

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

30	GCTACCTGAG	ATCAATAATG	CACTTGTAGT	CTATAAAAAT	GACGAAAATA	50
	AATCAAAAAT	CGTCCTTGAA	GTAGCTCTTG	AGCTTGGTGA	TGGAGTGGTT	100
	CGGACCATCG	CTATGGAATC	AACGGATGGG	TTGACTCGTG	GCATGGAAGT	150
	GCTAGATACT	GGTCGTCCAA	TTTCTGTGCC	AGTCGGCAAA	GAAACACTTG	200
35	GTCGCGTCTT	TAACGTTTTG	GGAGATACCA	TTGACTTGGA	TGCTCCTTTT	250
	GCGGATGATG	CAGAGCGCCA	GCCAATCCAT	AAGAAAGCTC	CAACCTTTGA	300
	TGAGTTGTCT	ACTTCATCAG	AGATCTTAGA	GACAGGTATC	AAGGTTATCG	350
	ACCTGTTAGC	ACCTTATCTG	AAAGGTGGTA	AAGTCGGACT	CTTCGGTGGT	400
	GCCGGAGTTG	GTAAGACCGT	CCTGATTCAG	GAATTGATCC	ACAACATTGC	450
40	CCAAGAGCAT	GGTGGTATTT	CCGTGTTTAC	CGGTGTTGGG	GAACGTACCC	500
	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AGGAGTCTGG	CGTTATCGAG	550
	AAAACAGCCA	TGGTCTTCGG	TCAGATGAAT	GAGCCACCAG	GAGCGCGTAT	600
	GCGGGTTGCT	TTGACTGGTT	TGACGATTGC	AGAGTACTTC	CGTGATGTAG	650
	AAGGTCAAGA	TGTCTTGCTC	TTCATTGACA	ACATCTTCCG	TTTCACGCAG	700
45	GCAGGTTCTG	AAGTCTCTGC	CCTTTTGGGT	CGGATGCCAT	CAGCCGTTGG	750
	TTACCAACCA	ACACTTGCGA	CTGAAATGGG	ACAACTCCAA	GAGCGTATTA	800
	CATCGACTAA	GAAAGGTTCT	GTAACCT			827

50 2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus oralis*

(B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

	GCAGCAGGGG	AAACACTTCC	TGAGATTAAT	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GTGATGGTAT	GGTCCGTACG	ATCGCCATGG	AATCAACAGA	TGGTTTGACT	150
10	CGTGGAATGG	AAGTTTGGGA	CACAGGCCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACTATTGACT	250
	TGGATGCTCC	TTTCGCTGAA	GACGCTGAGC	GTCAGCCAAT	TCATAAGAAA	300
	GCTCCAACCT	TTGATGAATT	GTCTACCTCA	TCTGAAATCT	TGGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGGAAAGTTG	400
15	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTGAT	CCAAGAGTTG	450
	ATTCACAACA	TTGCCCAAGA	ACATGGTGGT	ATTTTCAGTAT	TTACCGGTGT	500
	TGGAGAACGT	ACCCGTGAGG	GGAACGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCA	600
	CCTGGAGCAC	GTATGCGTGT	TGCTCTTACT	GGTTTGACAA	TCGCCGAATA	650
20	CTTCCGTGAT	GTAGAAGGCC	AAGATGTGCT	TCTCTTTATC	GACAATATCT	700
	TCCGTTTCAC	TCAAGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGGATG	750
	CCTTCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CTAAGAAGGG	TTCTGTAACC	TCTA	844

25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
45	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	250
	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300
	GCTCCAACCT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
50	GATCAAGGTT	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	500
	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
55	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
60	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG			830

2) INFORMATION FOR SEQ ID NO: 953

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 15 (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

20	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCTT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

2) INFORMATION FOR SEQ ID NO: 954

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAAC	TTGATGAG	TTGTACCT	CTCTGAA	AATCC	TTGAAAC	AGG	350
	GATCAAGG	TTTACCTT	CTTGCCC	CTTAAGG	GGTAAAG	TTG		400
	GACTTTTC	GGTGCCG	GATGGTA	AACTGT	CTTAAT	CCAAGA	ATTG	450
	ATTCACA	CAAGT	GCACGG	TGGT	ATTTCA	GAT	TTGCTG	500
5	TGGGGA	ACGT	ACTCGT	GAGG	GGAATG	ACCT	TTACTG	550
	CAGGCG	TTAT	CGAGAAA	ACA	GCCATG	GCT	TTGGTC	600
	CCAGGAG	CAC	GTATGCG	TGT	TGCCCT	TACT	GGTTTG	650
	CTTCCG	TGAT	GTGGAAG	GCC	AAGACG	TGCT	TCTCTT	700
	TCCGTT	TAC	TCAGGCT	TGGT	TCAGAA	GAT	CTGCCCT	750
10	CCATCAG	CCG	TTGGTT	ACCA	ACCAAC	ACTT	GCTACG	800
	GCAAGA	ACGT	ATCACAT	CAA	CCAAGA	AAGG	TTCTGT	844
							TCTA	

15 2) INFORMATION FOR SEQ ID NO: 955

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

30	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
35	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAAC	300
	TTGATGAGTT	GTCTACCTCT	CTCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTA	AAACCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
40	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
45	TCAGGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA		834

50 2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia microti*

(B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCATCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGGTTACACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Entamoeba histolytica*

(B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTCA	CAAGCATTAA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTATACTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTCAGGAC	GTCTTGCA	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGACGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

50 2) INFORMATION FOR SEQ ID NO: 958

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 bases

(B) TYPE: Nucleic acid

55 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

5	TACAACACCA	ACTTGCTAAA	TGGGCAGATG	CAGAAGTAGT	TGTTTATGTT	50
	GGTTGTGGGG	AACGTGGAAA	TGAAATGACC	GATGTACTTA	TGGAATTCCC	100
	AGAAATTATT	GACCCTAAGA	CAGGACAATC	TTTAATGAAG	AGAACAGTTC	150
	TTATAGCTAA	TACTTCTAAT	ATGCCAGTTG	CTGCTCGTGA	GGCTTCAATC	200
	TATACTGGTA	TAAC TATTGC	AGAATATTTT	AGAGATATGG	GATATTCAGT	250
10	GGCACTTATG	GCAGATTCAA	CAAGTCGTTG	GGCAGAAGCA	CTTCGTGAAA	300
	TGTCAGGACG	TTTGGAAGAA	ATGCCAGGTG	ATGAAGGATA	TCCAGCATAT	350
	CTATCAAGTA	GAATAGCAGA	GTTTTATGAA	AGAGCAGGGC	TTGTTGAATG	400
	TCTAGGTAAT	GGAGAAGAAG	GAGCATTAAAC	TGTAATTGGA	GCAGTATCTC	450
15	CA					452

2) INFORMATION FOR SEQ ID NO: 959

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
35	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACCGT	GATCAATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCCCTG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
40	GCTTCGTGAG	ATTTCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

2) INFORMATION FOR SEQ ID NO: 960

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

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5   TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGGTCATCT    50
    ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG    100
    TTCCCGACCC TGACGACCGT GATCGATGGT CGCGAGGAGT CGATCATGAA    150
    GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG    200
    AGGCCTCTAT TTACACCGGC ATCACCCTGG CCGAGTACTA CCGTGATATG    250
    GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC    300
    GCTTCGTGAG ATTTCTGGGTC GTTTGGCGGA GATGCCGGCC GATGGTGGCT    350
10  ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC    400
    CTCGTACCT  GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT    450
    CGGTGCCGTG TCTCCGCCG                                469

```

15

2) INFORMATION FOR SEQ ID NO: 961

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
- (B) STRAIN: ATCC 50126

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

```

35  TGTCATCAGT CAGGCCCTCT CCAAGTACTC CAACTCGGAC TGTGTCATCT    50
    ATGTCGGCTG CGGTGAACGC GGTAACGAGA TGGCCGAGGT GCTCATGGAG    100
    TTCCCGACCC TGACGACTGT GATCGATGGT CGCGAAGAGT CCATCATGAA    150
    GCGCACCTGC CTCGTGGCGA ACACCTCGAA CATGCCCGTC GCAGCCCGTG    200
    AGGCCTCTAT TTATACCGGC ATCACCCTTG CTGAGTACTA CCGTGATATG    250
    GGCAAGCACA TTGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC    300
    GCTGCGTGAG ATTTCTGGGTC GATTGGCGGA GATGCCGGCT GATGGTGGCT    350
    ACCCTGCCTA CCTCAGCGCC CGCCTCGCCT CCTTCTACGA GCGCGCCGGT    400
40  CTCGTACCT  GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATCGT    450
    CGGTGCAGTG TCTCCACCG                                469

```

45 2) INFORMATION FOR SEQ ID NO: 962

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
- (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

60

	TGTCATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAT	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACCGT	GATCGATGGC	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCAGTC	GCAGCCCCGTG	200
5	AGGCCTCTAT	TTACACCGGC	ATCACCTTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCTGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCCGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
10	CGGTGCCGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 963

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

30	TGTGATCAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCGGAC	TGCGTCATCT	50
	ACGTCGGCTG	TGGTGAGCGC	GGGAACGAGA	TGGCCGAGGT	GCTCATGGAT	100
	TTCCCGACTT	TGACGACTGT	GATCGATGGT	CGCGAGGAGT	CCATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCCAA	CATGCCAGTT	GCAGCCCCGTG	200
	AGGCTTCTAT	CTATACCGGC	ATCACACTGG	CTGAGTACTA	TCGTGATATG	250
35	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GTTGCGTGAG	ATTTCCGGTC	GGCTGGCGGA	GATGCCGGCC	GATGGTGGTT	350
	ACCCCGCCTA	CCTCAGTGCC	CGTCTCGCCT	CCTTCTACGA	GCGCGCTGGC	400
	CTCGTGACCT	GTATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACAATTGT	450
40	TGGTGCGGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 964

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

60	GGTCATTAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCTGAC	TGCGTCATCT	50
	ACGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100

	TTCCCCGACCC	TGACGACCAT	GATCGATGGT	CGGGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	CTACACCGGC	ATCACCTCG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCTGAGGC	300
5	GCTTCGTGAG	ATTTCTGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCCCGTG	TCTCCGCCG				469

10

2) INFORMATION FOR SEQ ID NO: 965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
30	TTCCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCTGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
35	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCCGTG	TCTCCGCCG				469

40

2) INFORMATION FOR SEQ ID NO: 966

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 449 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

	CACCA GTTCG	CCAAGTGGGC	AGATGCTCAG	ATAGTTGTAT	ACGTTGGTTG	50
	TGGAGAACGT	GGTAACGAGA	TGACAGACGT	TCTAAATGAA	TTCCCAGAAC	100
	TGATTGACCC	TCATACAGGC	GAATCTCTAA	TGAAGAGAAC	AGTTCTTATA	150
60	GCTAATACGT	CAAATATGCC	AGTTGCAGCC	AGAGAGGCAA	GTATATATAC	200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCACC	449

2) INFORMATION FOR SEQ ID NO: 967

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: ATCC 9797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGCAGA	CGGCCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCG	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCCTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTC	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCG	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCGA	CGGTGCGTTC	CTGATGCCCG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCGTG	GCACGGTGGT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	CGTGGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGTTC	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGTACATT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTCACACG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGGCGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

45 2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: BD180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

60

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CGATCCTGGT GGTGTCGGCC GCAGACGGCC CGATGCCGCA GACGCGCGAG      50
CACATTTTGC TGTGCGGCCA GGTGCGCGTG CCGTACATCA TCGTGTTTCT      100
GAACAAGGCG GACATGGTTG ATGACGCGGA GCTGCTCGAG CTGGTGGAGA      150
TGGAAGTCCG CGAACTGCTG AGCAAGTACG ATTTCCCGGG CGATGACACG      200
5 CCGATCGTGA AGGGTTCGGC CAAGCTGGCG CTGGAAGGCG ACAAGGGCGA      250
ACTGGGCGAG CAGGCGATTG TGTCGCTGGC GCAAGCGCTG GACACGTACA      300
TTCCGACGCC GGAGCGCGCG GTCGACGGTG CGTTCCTGAT GCCGGTGGAA      350
GACGTGTTCT CGATCTCGGG CCGTGGCAGG GTGGTGA CTG GCGGTATCGA      400
GCGCGGCGTG GTGAAGGTTG GCGAGGAAAT CGAAATCGTG GGCATCAAGC      450
10 CGACGGTGAA GACGACCTGC ACGGGCGTGG AGATGTTCCG CAAGCTGCTG      500
GACCAGGGCC AGGCGGGCGA CAACGTGGGT ATCTTGCTGC GCGGCACCAA      550
GCGTGAAGAC GTCGAGCGTG GCCAGGTGCT GGCCAAGCCG GGTTCGATCA      600
ACCCGCACAC GGACTTCACG GCCGAGGTGT ACATTCTGTC CAAGGAAGAG      650
GGTGGCCGTC ACACGCCGTT CTTCAACGGC TATCGTCCGC AGTTCTACTT      700
15 CCGCACGACG GACGTGACCG GCACGATCGA CCTGCCGGCG GACAAGGAAA      750
TGGTGCTGCC GGGCGACAAC GTGTCGATGA CCGTCAAGCT GCTGGCCCCG      800
ATCGCCATGG AAGAAGG      817

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20

2) INFORMATION FOR SEQ ID NO: 969

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 637 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus columbae*
- (B) STRAIN: ATCC 51263

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

```

CCTATGCCAC AAACCTCGTGA ACACATTCTT TTATCACGTA ACGTTGGTGT      50
GCCATACATC GTTGTTTTCT TAAACAAAGT TGATATGGTT GACGACGAAG      100
AATTATTAGA ATTAGTTGAA ATGGAAGTTC GTGACTTATT AACTGAATAT      150
40 GACTTCCAG GAGACGATGT TCCTGTAATC GCTGGTTCTG CATTAAAAGC      200
TTTAGAAGGC GACCCTGCTT ACGAAGAAAA AATCTTAGAA TTAATGGCTG      250
CAGTTGACGA ATACATCCCA ACTCCAGAAC GTGACAACGA CAAACCATTC      300
ATGATGCCAG TTGAAGACGT GTTCTCAATT ACTGGTCGTG GTACTGTTGC      350
TACAGGTCGT GTTGAACGTG GACAAGTTCG TGTTGGTGAC GAAGTTGAAA      400
45 TCGTTGGTAT CGCTGACGAA ACTTCTAAAA CAACAGTTAC TGGTGTGAA      450
ATGTTCCGTA AATTATTAGA TTACGCTGAA GCTGGAGACA ACATCGGTGC      500
ATTATTACGT GGTGTGGCTC GTGAAGACAT CCAACGTGGT CAAGTATTAG      550
CTAAACCAGG TTCAATCACT CCACATACAA AATTCCTGCT TGAAGTGTAC      600
GTTTAACTA AAGAAGAAGG TGGACGTCAT ACTCCAT      637
50

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2) INFORMATION FOR SEQ ID NO: 970

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 634 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

5 (B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

	TATGCCTCAA	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	50
10	CATACATCGT	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	150
	CTTCCCAGGC	GACGATGTTT	CTGTAATCGC	TGGTCTGCT	TTGAAAGCTC	200
	TTGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	250
	GTTGACGAAT	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	300
15	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGAAAC	TGCTAAAACA	ACTGTAAGT	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	500
	TGCTACGTGG	GGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTAGCT	550
20	AAAGCTGGTA	CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	600
	TTTAACAAAA	GAAGAAGGTG	GACGTCACAC	TCCA		634

25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

40	GGACCAATGC	CACAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTTGG	50
	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	AGTTGACTTG	GTTGACGACG	100
	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	TCCGTGACCT	ATTGTCAGAA	150
	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	ATCCAAGGTT	CAGCACTTAA	200
45	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	CATCGTTATG	GAATTGATGA	250
	ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	300
	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	ATCACTGGAC	GTGGTACAGT	350
	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	TAAAGTCAAC	GACGAAATCG	400
	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	AAGCAGTTGT	TACTGGTGT	450
50	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	500
	TGTCCTTCTT	CGTGGTGTTC	AACGTGATGA	AATCGAACGT	GGACAAGTTA	550
	TCGCTAAACC	AGGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTC	600
	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	650
	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	TGACGTTACA	GGTTCAATCG	700
55	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	CTGGTGATAA	CGTGACAATC	750
	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	GAACAAG		787

60 2) INFORMATION FOR SEQ ID NO: 972

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

15	TAGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	GCACATCCTG	50
	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	TGAACAAATG	100
	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTTGAA	ATGGAAGTTC	150
	GTGAACCTCT	GTCTCAGTAC	GACTTCCCGG	GCGACGACAC	TCCGATCGTT	200
20	CGTGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GACGCAGAGT	GGGAAGCGAA	250
	AATCCTGGAA	CTGGCTGGCT	TCCTGGATTC	TTACATTCCG	GAACCAGAGC	300
	GTGCGATTGA	CAAGCCGTTT	CTGCTGCCGA	TCGAAGACGT	ATTCTCCATC	350
	TCCGGTCGTC	GTACCGTTGT	TACCGGTCGT	GTAGAACGCG	GTATCATCAA	400
	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGAGACT	CAGAAGTCTA	450
25	CCTGTACTGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	AGGCCGTGCT	500
	GGTGAGAACG	TAGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	AAGAAATCGA	550
	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCAC	CATCAAGCCG	CACACCAAGT	600
	TCGAATCTGA	AGTGATACAT	CTGTCCAAAG	ATGAAGGCCG	CCGTCATACT	650
	CCGTTCTTCA	AAGGCTACCG	TCCGCAAGTC	TACTTCCGTA	CTACTGACGT	700
30	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	ATGCCGGGCG	750
	ACAACATCAA	AATGGTTGTT	ACCCTGATCC	ACCCGATCGC	GATGGACGAC	800
	GGT					803

2) INFORMATION FOR SEQ ID NO: 973

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

55	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	CACATCCTGC	TGGGTCGTCA	50
	GGTAGGCGTT	CCGTACATCA	TCGTGTTTCT	GAACAAATGC	GACATGGTTG	100
	ATGACGAAGA	GCTGCTGGAA	CTGGTTGAAA	TGGAAGTTTC	TGAACCTCTG	150
	TCTCAGTACG	ACTTCCCGGG	CGACGACACT	CCGATCGTTC	GTGGTTCTGC	200
	TCTGAAAGCG	CTGGAAGGCG	ACGCAGAGTG	GGAAGCGAAA	ATCCTGGAAC	250
	TGGCTGGCTT	CCTGGATTCC	TACATTCCGG	AACCAGAGCG	TGCRATTGAC	300
	AAGCCGTTCC	TGCTGCCGAT	CGAAGACGTA	TTCTCCATCT	CCGGTCGTGG	350
	TACCGTTGTT	ACCGGTCGTG	TAGAACGCGG	TATCATCAA	GTTGGTGAAG	400
60	AAGTTGAAAT	CGTTGGTATC	AAAGAGACTC	AGAAGTCTAC	CTGTACTGGC	450

GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	GGCCGTGCTG	GTGAGAACGT	500
AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	AGAAATCGAA	CGTGGTCAGG	550
TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	ACACCAAGTT	CGAATCTGAA	600
GTGTACATTC	TGTCCAAAGA	TGAAGGCGGC	CGTCATACTC	CGTTCTTCAA	650
5 AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	TACTGACGTG	ACTGGTACCA	700
TTGAACTGCC	GGAAGGCGTA	GAGATGGTAA	TGCCGGGCGA	CAACATCAAA	750
ATGGTTGTTA	CC				762

10

2) INFORMATION FOR SEQ ID NO: 974

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 11775

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
TCCTGCTGGG	TCGTCAGGTA	GGCGTTCGGT	ACATCATCGT	GTTCTGAAC	100
AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
30 AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
TCGTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCCTACA	TTCCGGAACC	300
AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
35 ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GCGGTATCAA	ACGTGAAGAA	550
ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGTCGTC	650
40 ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
ACGA					804

45

2) INFORMATION FOR SEQ ID NO: 975

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

	GCGATCCTGG	TAGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
5	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GACTTCCCGG	GCGACGACAC	200
	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GACGCAGAGT	250
	GGGAAGCGAA	AATCCTGGAA	CTGGCTGGCT	TCCTGGATTC	YTACATTCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTT	CTGCTGCCGA	TCGAAGACGT	350
10	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAGAACGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGAGACT	450
	CAGAAGTCTA	CCTGTACTGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TAGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCAC	CATCAAGCCG	600
15	CACACCAAGT	TCGAATCTGA	AGTGTACATT	CTGTCCAAAG	ATGAAGGCGG	650
	TCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGTGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATCAA	AATGGTTGTT	ACCCTGATCC	ACCCGATCGC	800
20	GATG					804

2) INFORMATION FOR SEQ ID NO: 976

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
 (B) STRAIN: Mavi-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

	GGCGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CGCAGACCCG	50
40	TGAGCACGTG	CTGCTCGCCC	GTCAGGTCGG	TGTGCCCTAC	ATCCTGGTCG	100
	CCCTGAACAA	GGCCGACATG	GTCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCCGCC	CAGGAGTTCG	ACGAGGACGC	200
	CCCGGTGGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGC	GACGCCAAGT	250
	GGGTGCGAGTC	CGTCGAGCAG	CTGATGGAGG	CCGTGACGCA	GTCGATCCCG	300
45	GACCCGGTCC	GCGAGACGGA	GAAGCCGTTT	CTGATGCCGG	TGGAGGACGT	350
	CTTCACCATC	ACCGGGCGTG	GCACCGTGGT	CACCGGTCGT	GTCGAGCGCG	400
	GTGTGATCAA	CGTGAACGAG	GAAGTCGAGA	TCGTGCGCAT	CCGCCCCGAC	450
	AGCACCAAGA	CCACGGTCAC	CGGTGTGGAR	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTATCAAGC	550
50	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTGA	CCAAGCCCGG	CACCACCACG	600
	CCGCACACCG	AGTTCGAGGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCGT	800
55	CGCCATGGAC	GACGGTSTGC	GGTTC			825

2) INFORMATION FOR SEQ ID NO: 977

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

```

15  TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
    ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG      100
    AACAAAGTTG ACTTG GTTGA CGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
    GGAAATCCGT GACCTATTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
    CAGTTATCCA AGGTTTCAGCA CTTAAAGCTC TTGAAGGTGA CTCTAAATAC      250
20  GAAGACATCG TTATGGAATT GATGAACACA GTTGATGAGT ATATCCCAGA      300
    ACCAGAACGT GACACTGACA AACCATTGCT TCTTCCAGTC GAGGACGTAT      350
    TCTCAATCAC TGGACGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
    ATCGTTAAAG TCAACGACGA AATCGAAATT GTTGGTATCA AAGAAGAAAC      450
    TCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAC CAACTTGACG      500
25  AAGGTCTTGC TGGAGATAAC GTAGGTGTCC TTCTTCGTGG TGTTCAACGT      550
    GATGAAATCG AACGTGGACA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
    ACACACTAAA TTCAAAGGTG AAGTCTACAT CTTACTAAA GAAGAAGGTG      650
    GACGTCACAC TCCATTCTTC AACAACTACC GTCCACAATT CTACTTCCGT      700
    ACTACTGACG TTACAGGTTT AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
30  AATGCCTGGT GATAACGTGA CAATCGACGT TGAGTTGATT CACCCAATCG      800
    CCGTAGAACA AGGTACTACA
  
```

2) INFORMATION FOR SEQ ID NO: 978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

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50  GGCGCGATCC TGGTGGTCGC CGCCACCGAT GGCCCGATGC CGCAGACCCG      50
    TGAGCACGTG CTGCTCGCCC GTCAGGTGGG CGTGCCCTAC ATCCTGGTGG      100
    CGCTGAACAA GTCCGACGCG GTCGACGACG AGGAGCTGCT CGAGCTCGTC      150
    GAGCTGGAGG TCCGCGAGTT GCTGGCCGCC CAGGACTTCG ACGAGGAAGC      200
55  TCCGGTGGTC CGGGTCTCGG CGCTGAAGGC GCTCGAGGGC GACGCCACCT      250
    GGGTGAAGTC GGTAGAGGAC TTGATGGACG CGGTCGACGA GTCGATTCCG      300
    GACCCGGTCC GCGACACCGA CAAGCCGTTT CTGATGCCCG TCGAGGACGT      350
    CTTCAACATC ACCGGTCGTG GCACCGTCGT CACCGGCCGT GTGGAGCGCG      400
    GCGTGGTGAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CAAGCCGACC      450
60  AGCACCAAGA CCACGGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
  
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CCAGGGTCAG GCCGGTGACA ACGTCGGTCT GCTGCTGCGT GGTGTCAAGC 550
GTGAGGACGT CGAGCGCGGC CAGGTCGTCA TCAAGCCCGG CACCACCACT 600
CCGCACACCG AGTTCGAGGG TCAGGTCTAC ATCCTGTCCA AGGACGAGGG 650
CGGCCGGCAC ACGCCGTTCT TCAACAAC TA CCGTCCGCAG TTCTACTTCC 700
5 GCACCACCGA CGTGACCGGT GTGGTGACGC TGCCGGAGGG CACCGAAATG 750
GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGCTGA TCCAGCCCGT 800
CGCCATGGAC GACGGTCTGC GG 822

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2) INFORMATION FOR SEQ ID NO: 979

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-11

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

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CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG 50
CACATCCTTC TTTCACGTCA GGTGTTGGTGT AAACACCTTA TCGTCTTCAT 100
GAACAAAGTT GACTTGTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA 150
30 TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT 200
CCAGTTATCC AAGGTTTCAGC ACTTAAAGCT CTTGAAGGTG ACTCTAAATA 250
CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TATATCCCAG 300
AACCAGAACG TGACACTGAC AAACCATTCG TTCTTCCAGT CGAGGACGTA 350
TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
35 TATCGTTAAA GTCAACGACG AAATCGAAAT CGTTGGTATC AAAGAAGAAA 450
CTCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500
GAAGGTCTTG CTGGAGATAA CGTAGGTGTC CTTCTTCGTG GTGTTCAACG 550
TGATGAAATC GAACGTGGAC AAGTTATCGC TAAACCAGGT TCAATCAACC 600
CACACACTAA ATTCAAAGGT GAAGTCTACA TCCTTACTAA AGAAGAAGGT 650
40 GGACGTCACA CTCCATTCTT CAACAAC TACGTCACAAT TCTACTTCCG 700
TACTACTGAC GTTACAGGT CAATCGAACT TCCAGCAGGT ACTGAAATGG 750
TAATGCCTGG TGATAACGTG ACAATCGACG TTGAGTTGAT TCACCCAATC 800
GCCGTAGAAC AAGGTACTAC A 821

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2) INFORMATION FOR SEQ ID NO: 980

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: ATCC 25177

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCAGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
5	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCT	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCGG	TCGAGGACGT	350
10	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCCGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCGGGCGACA	ACGTGGGTTT	GCTGCTGCGG	GGCGTCAAGC	550
	GCGAGGACGT	CGAGCGTGCG	CAGGTTGTCA	CCTAGCCCGG	CACCAACACG	600
15	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGCGAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
20	CGCCATGGAC	GAAGGTNTGC	GTTTCGCG			828

2) INFORMATION FOR SEQ ID NO: 981

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGCCCAATG	CCACAAACTC	50
40	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
45	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTT	550
50	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTAATCGCTC	800
55	CAATCGCGAT	TGAAGACGG				819

2) INFORMATION FOR SEQ ID NO: 982

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

15	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAGATC	GACTTGGTTG	ATGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTCTTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCT	CTTGAAGGTG	ATACTAAGTA	250
20	CGAAGACATC	ATCATGGAAT	TGATGAACAC	TGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTCTTC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGATG	AAATCGAAAT	CGTTGGGTATC	AAAGAAGAAA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAGCTTGAC	500
25	GAAGGTCTTG	CAGGGGACAA	CGTAGGTGTA	CTTCTTCGTG	GTATCCAACG	550
	TGATGAAATC	GAACGTGGTC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAGGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAGT	TCTACTTCCG	700
	TACAACCTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
30	TAATGCCTGG	TGATAACGTA	ACTATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTTGAAC	AAGG				814

2) INFORMATION FOR SEQ ID NO: 983

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

50	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
55	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGGTATC	AAAGAAGAAA	450
60	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500

	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
5	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC					810

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2) INFORMATION FOR SEQ ID NO: 984

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

	TCCTTGTAGT	AGCTTCAACT	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCCTTCTTT	CACGTCAGGT	TGGTGTTAAA	CACCTTATCG	TCTTCATGAA	100
	CAAGATCGAC	TTGGTTGATG	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	150
30	AAATCCGTGA	CCTCTTGTC	GAATACGACT	TCCAGGTGA	CGATCTTCCA	200
	GTTATCCAAG	GTTTCAGCTCT	TAAAGCTCTT	GAAGGTGATA	CTAAGTACGA	250
	AGACATCATC	ATGGAATTGA	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	300
	CAGAACGTGA	TACTGACAAA	CCTCTTCTTC	TTCCAGTCGA	AGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	400
35	TGTTTCGTGTC	AACGATGAAA	TCGAAATCGT	TGGTATCAAA	GAAGAAATCC	450
	AAAAAGCAGT	TGTTACTGGT	GTTGAAATGT	TCCGTAAACA	GCTTGACGAA	500
	GGTCTTGCA	GGGACAACGT	AGGTGTACTT	CTTCGTGGTA	TCCAACGTGA	550
	TGAAATCGAA	CGTGGTCAAG	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	600
	ACACTAAATT	CAAGGGTGAA	GTTTACATCC	TTACTAAAGA	AGAAGGTGGA	650
40	CGTCACACTC	CATTCTTCAA	CAACTACCGT	CCACAGTTCT	ACTTCCGTAC	700
	AACTGACGTT	ACAGGTTCAA	TCGAACTTCC	AGCAGGTACT	GAAATGGTAA	750
	TGCCTGGTGA	TAACGTAAC	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	800
	GTTGAACAAG	GTACTAC				817

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2) INFORMATION FOR SEQ ID NO: 985

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTTAAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTCA	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	GTTCAGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCGA	AGACGTATTC	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTTCGTGTC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTC	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACCTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	GTAGAACAAG	GTACTACA	798

20

2) INFORMATION FOR SEQ ID NO: 986

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
	CTTCTTTCAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	800
55	GAACAAGGTA	CTACA				815

2) INFORMATION FOR SEQ ID NO: 987

60 (i) SEQUENCE CHARACTERISTICS:

549

- (A) LENGTH: 832 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Enterococcus hirae*
- (B) STRAIN: ATCC 8043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
15	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAA	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCAAA	GAGCCGTAGT	AACAGGAGTT	GAAATGTTCC	GCAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGGTTCAATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTTGA	CTAAAGAAGA	650
	AGGCGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAACA	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Enterococcus mundtii*
- (B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCGATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTCGTGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCGTGTCGG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTT	CGTAAAACGT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACCGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTAGTATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCCTGTTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCATT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTCGTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTTCAGTG	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	TTTAACAAC	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTAAGTAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTTCTCTA	TT		832

45 2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

	GGATCCTGTA	TATGCACAAA	AACTAGGTGT	TAACATCGAT	GAATTACTAT	50
	TATCACAACC	TGATACAGGG	GAGCAAGGTT	TAGAAATCGC	AGAAGCACTT	100
5	GTACGAAGTG	GTGCGGTTGA	TATTATCGTA	ATTGACTCTG	TAGCAGCTCT	150
	TGTA					154

2) INFORMATION FOR SEQ ID NO: 991

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25	GCCATTGCAG	AGGCACAGAA	GCAGGGCGGT	ATTGCAGCCT	TCATTGATGC	50
	TGAGCACGCC	TTCGACCGTT	TCTATGCAGA	GAAGTTAGGT	GTGGATGTTG	100
	ATAACCTTTG	GGTTTCACAG	CCAGACAATG	GTGAGCAGGC	TTTAGAGATT	150
	GCCGACCAGC	TGATTCGCTC	TTCCGCTATT	GACATTCTCG	TTGTCGACTC	200
	AGTTGCAGCC	TTGACTCCAA	AGAAGGAGAT	TGAGGGTGAC	ATGGGTGACT	250
30	CTGCAGTAGG	TTTACAAGCA	CGACTGATGA	GTCAGGCATT	GCGTAAACTT	300
	ACCTCAACAA	TCGCAAAAAC	TAATACTTGC	TGCATCTTCA	TCAACCAGTT	350
	GCGTGAGAAG	ATTGGTGTGA	TGTTTGGTAA	TCCA		384

35

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 624 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R760

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	CATACATCGT	50
	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	TTACTAGAAT	100
	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	CTTCCCAGGC	150
55	GACGATGTTT	CTGTAATCGC	TGGTTCTGCT	TTGAAAGCTC	TTGAAGGCGA	200
	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	GTTGACGAAT	250
	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTCAT	GATGCCAGTC	300
	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	CAGGCCGTGT	350
	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	GTTGGTATTG	400
60	CTGAAGAAAC	TGCTAAAACA	ACTGTAAGTG	GTGTTGAAAT	GTTCCGTAAA	450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGGTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: extracted from U40453

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

ATGGAAAACA	ATAAAAAAGT	ATTGAAGAAA	ATGGTATTTT	TTGTTTTAGT	50
GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
CCGATCCAAG	CCAAC TTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
ATATATTTTC	TTTATGAGGG	TGACCCTGTT	ACTCACGAGA	ATGTGAAATC	200
TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
ATTATGATAA	ATTAAAAACT	GAACCTAAGA	ACCAAGAGAT	GGCAACTTTA	300
TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
TTATTTATGT	GAAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGTTAAA	450
GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
TATATAAAGT	TCATACCTAA	GAATAAAGAA	AGTTTTTTGGT	TTGATTTTTT	650
CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACAACC	750
AAGTAA					756

40

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995

ACATTCTCGT GAGTAACAGG GT

2) INFORMATION FOR SEQ ID NO: 996

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996

ACAAATCATG AAGGGAATCA TTTAG

2) INFORMATION FOR SEQ ID NO: 997

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997

CTAATTCTTG AGCAGTTACC ATT

2) INFORMATION FOR SEQ ID NO: 998

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998

GGAGGGGTAA CAAATCATGA AGG

2) INFORMATION FOR SEQ ID NO: 999

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999

15 TTGACCTTGT TGATGACGAA GAG

23

2) INFORMATION FOR SEQ ID NO: 1000

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000

30

TTAGTGTGTG GGTTGATTGA ACT

23

2) INFORMATION FOR SEQ ID NO: 1001

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001

AAGAGTTGCT TGAATTAGTT GAG

23

2) INFORMATION FOR SEQ ID NO: 1002

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

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AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC      50
TTCAACTGAT GGACCAATGC CACAAACTCG TGAGCACATC CTTCTTTCAC      100
GTCAGGTTGG TGTTAAACAC CTTATCGTGT TCATGAACAA AGTTGACCTT      150
10 GTTGATGACG AAGAGTTGCT TGAATTAGTT GAGATGGAAA TTCGTGACCT      200
TCTTTCAGAA TACGATTTCC CAGGTGATGA CCTTCCAGTT ATCCAAGGTT      250
CAGCTCTTAA AGCTCTTGAA GGCGACACTA AATTTGAAGA CATCATCATG      300
GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC      350
TGACAAACCA TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC      400
15 GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTACTGT TCGTGTCAAC      450
GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTAAAA AAGCTGTTGT      500
TACTGGTGTG GAAATGTTCC GTAAACAAC TACGGAAGGT CTTGCAGGAG      550
ACAACGTAGG TATCCTTCTT CGTGGTGTTC AACGTGACGA AATCGAACGT      600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCACACA CTAAATTCAA      650
20 AGGTGAAGTA TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT      700
TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACAAC TGACGTAACA      750
GGTTCAATCG AACTTCCAGC AGGTACAGAA ATGGTTATGC CTGGTGATAA      800
CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA GAACAAGGTA      850
CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT          894
25

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2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

40 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

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AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTAC      50
45 TATTATCACA GCCTGATACA GGGGAGCAAG GATTAGAAAT CGCGGAAGCA      100
CTTGTAACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC      150
TCTTGTACCG AAAGCAGAGA TTGAAGGCGA CATGGGTGAC TCACACGTAG      200
GTTTACAAGC ACGTTTAAATG TCACAAGCAC TTCGTAAGCT TTCAGGAGCA      250
ATCAACAAAT CAAAAACAAT TGCAATCTTT ATTAACCAAA TTCGTGAAAA      300
50 AGTTGGGGTT ATGTTTCGGAA ACCCAGAAAC AA          332

```

2) INFORMATION FOR SEQ ID NO: 1004

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

10	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAAC TC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
15	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
20	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
25	CTCAAGCTGG	TAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
30	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CC				1212

2) INFORMATION FOR SEQ ID NO: 1005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

55	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
60	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTCGGTAA	TATTACTCTG	350

	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCGAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCGTGG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
55	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACCTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
25	ACGTTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
30	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
35	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
40	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
45	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCTGATC				1218

50 2) INFORMATION FOR SEQ ID NO: 1008

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1223 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

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5   GTAGACCAAG AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA      50
    ATACGTCTCT TACCCTGACG ATGATTTGCA AGTCGCATCT ACGGTCGTAG      100
    ATGTTTCAAA TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA      150
    AGTAACGTTT CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG      200
10  GGGTTCTGCT ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG      250
    GTGTTTATGA TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT      300
    CCGGGAACAA GCACACCTGT CTACAACCTGG GATAGAGCAT ATTTTCGGTAA      350
    TATTACTCTG CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG      400
    AGACTTTGAA TAAGGTCGGT CTAGATAGAG CTAAAACCTT CCTTAATGGT      450
15  CTTGGTATCG ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA      500
    TACAACAGAA TCTAATAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG      550
    CTGCTTATGC TGCCTTTGCA AATGGTGGCA CTTACTATAA ACCAATGTAT      600
    ATCCATAAAG TCGTCTTCAG TGATGGAAGT AAAAAAGAGT TCTCTAATGT      650
    CGGAACTCGT GCCATGAAGG AAACGACAGC CTATATGATG ACCGACATGA      700
20  TGAAAACAGT CTTGACTTAT GGAAGTGGGC GTGGAGCCTA TCTTCCTTGG      750
    CTTCTCAAG CTGGTAAAC AGGAACCTCT AACTATACAG ATGAGGAAGT      800
    TGAAAACCAC ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG      850
    TTGGTTATAC TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCGAAT      900
    CGTTTAACTC CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA      950
25  TCGCTCAATG ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA     1000
    CGATGCCAGA CGGACTTTTC AGAAACGGGG AATTTGTATT CAAAAATGGA     1050
    GCTCGCCCAA TATGGACTGA ACCCTCTACT CAACAATCCT CAACAGCTGA     1100
    AAGTTCAAGC TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA     1150
    CTCCAAGCAC AAATAATAGT ACGACTACCA ATCCTAACAA TAATACGCAA     1200
30  CAATCAAATA CAACCCCTGA TCA                                     1223
  
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2) INFORMATION FOR SEQ ID NO: 1009

35

(i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 1214 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
40  (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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45  (A) ORGANISM: Streptococcus pneumoniae
    (B) STRAIN: StrR-06
  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

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50  ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAATCT CGATCAATAC      50
    GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
    TTCAAATGGT AAAGTCATCG CCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
    ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGACTGGGGT      200
    TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
55  TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
    GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT      350
    ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
    TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
    GTATCGAGTA TCCAAGCATG CATTATGCAA ACGCCATTTT AAGTAATACA      500
60  ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550
  
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	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCT				1214
15						

2) INFORMATION FOR SEQ ID NO: 1010

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1223 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-07
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAACCTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTCATTC	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTGGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTCTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGACTACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTC	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAAATCGTC	TTTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTG	AGCTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACCTTCA	AGTCTAACTC	AACCACTCCA	1150
	AGCACAAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

60

2) INFORMATION FOR SEQ ID NO: 1011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCTTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
20	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCGGTAA	TATTACTCTG	350
25	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
30	TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGT	650
	GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	TGAAAACAGT	700
	CTTGACTTAT	GGAACCTGGC	GTGGAGCCTA	TCTTCCTTGG	CTTCCTCAAG	750
	CTGGTAAAAC	AGGAACCTCT	AACATAACAG	ATGAGGAAGT	TGAAAACCAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
35	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGCCCAA	1050
	TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	AAGTTCAAGC	1100
40	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCC					1207

2) INFORMATION FOR SEQ ID NO: 1012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
5	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGA CTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACA ACTGG	GATAGAGCAT	ATTTCCGGTAA	TATTACTCTG	350
	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
10	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAA	TTTCAGATGT	AGGTACACGA	650
15	GCTATGAAAG	AAACA ACTGC	TTACATGATG	ACCGAAATGA	TGAAA ACTGT	700
	CTTGGCATAC	GGAACTGGTC	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATT CGAAT	CGTTTAACTC	900
20	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGTTCTA	1050
	CGTGGA ACTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
25	AAATAATAGT	ACGACTACCG	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	C					1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1220 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATCTAC	AACTCCGATC	50
	AATACGTCTC	TTACCCTGAC	GATGATTTGC	AAGTCGCATC	TACGGTCGTA	100
	GATGTTTCAA	ATGGTAAAGT	CATCGCACAA	CTTGGTGCTC	GTCATCAAGC	150
	AAGTAATGTT	TCATTCCGGTA	CCAACCAGGC	CGTAGAAACC	AATCGTGA CT	200
50	GGGGATCATC	AATGAAACCA	ATCACTGA CT	ATGCTCCCGC	TTTAGAATAT	250
	GGAGTCTATG	ACTCTACTGC	TTCTATTGTA	CATGATGTCC	CTTATAACTA	300
	TCCTGGCACT	GATACTCCAC	TCTACA ACTG	GGATCATGTC	TACTTTGGAA	350
	ACATTACAAT	CCAGTATGCT	CTTCAACAAT	CACGAAATGT	CACAGCCGTT	400
	GAGACTTTGA	ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TCCTTAATGG	450
55	TCTTGGTATC	GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	500
	ACACAACTGA	ATCCAACAAA	AAATATGGTG	CAAGTAGTGA	AAAAATGGCT	550
	GCTGCCTACG	CTGCTTTTGC	TAATGGTGGT	ATTTATCACA	AACCAATGTA	600
	TATCAATAAA	ATCGTCTTTA	GTGATGGTAG	CGAAAAAGAA	TTTTCTGATG	650
	CTGGTACACG	AGCTATGAAA	GAGACTACTG	CCTATATGAT	GACTGAAATG	700
60	ATGAAA ACTG	TTTTAACTTA	CGGAACAGGA	CGTGGAGCCT	ACCTACCATG	750

	GCTTCCACAA	GCAGGTAAGA	CAGGTA CTTC	TAACTATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATAACCAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TTAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAACCT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	500
40	CAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGCCGA	CATGATGAAA	ACTGTCTTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CCTGGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	CTCCACAACA	ACCCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

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2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 bases

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- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCCGGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACACACAG	ATGATGAAAT	TGAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATAACAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

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2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAAC	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACTGG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	CACAACTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCCTACGC	TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACGTG	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCGAT	GAAATGTTTG	850
	TGGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCAG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGAGGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCCAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCACTA	CTCAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGA	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTCGTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGGT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACCTACACA	GATGATGAAA	800
	TTGAAAAACA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTCTGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCA	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAAC	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCCTGCCGT	400
	TGAAACACTA	AACAAGGTTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTCAC	ACTCAAATGC	TATTTCAAGT	500
35	AATACAAC	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTTC	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATAA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTA	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACTGGCTAC	GTAGCTCCAG	ATGAAATGTT	850
	TGTGGGTTAT	ACTCGTAAGT	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAAC	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAGTGG	AGAATTTCGTA	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
	AACAATCAAA	TACAACCCCT	GATCA			1225

2) INFORMATION FOR SEQ ID NO: 1019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

5 (B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

10	GCCTCTATTT	CAAAGGAGAT	GCCTGGCATT	AGTATTTCTA	CTTCTTGGGA	50
	TCGAAAGGTT	TTGGAAACTT	CCCTTTCTTC	TATAGTAGGG	AGTGTATCCA	100
	GTGAAAAAGC	TGGTCTCCCA	GCGGAAGAAG	CAGAATCCTA	TCTTAAAAAA	150
	GGCTATTCTC	TAAATGACCG	TGTTGGAACC	TCCTATTTGG	AAAAGCAATA	200
	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
15	AACAATATCA	AAC TGACCAT	TGATT TGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCAGGT	TCGGTTGTCA	550
20	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTTC	CAAGGTTTCA	CTCCAATTTA	650
	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
25	AACAGCTATG	GGAAAACTTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAAA	900
	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
30	AAGGGAGGAC	TGGGTGACTT	GATTTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
35	CATCTGATAA	TCCCCAAATC	GCTGTGCGAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTA		1439

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2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1441 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

60	GCCTCTATTT	CAAAGGAGAT	GCCTGGCATT	AGTATTTCTA	CTTCTTGGGA	50
	TCGAAAGGTT	TTGGAAACTT	CCCTTTCTTC	TATAGTAGGG	AGTGTATCCA	100
	GTGAAAAAGC	TGGTCTCCCA	GCGGAAGAAG	CAGAATCCTA	TCTTAAAAAA	150
	GGCTATTCTC	TAAATGACCG	TGTTGGAACC	TCCTATTTGG	AAAAGCAATA	200

	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTCAG	CTCCAATTTA	650
10	TTCTTGATAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGAGATA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAAACCTT	CTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CGATGCAAT	CTACTGGATT	TGTTCCCAAA	900
15	GAGTATAGCT	TTGCTAATTA	CATACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTGCGAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAACTAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCTTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800

	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

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2) INFORMATION FOR SEQ ID NO: 1022

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1428 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATTG	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAAACTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTTGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTTGGCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCAAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCTTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCAGGTT	CGGTTGTCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTTA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTCC	AAGTTTCAGC	TCCAATTTAT	TCTTGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGAGATAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGAAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACAG	CAATTTGGAA	ACAGCTATGG	800
	GAAAACTTCG	TGCGACCTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATTT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTCGTGTG	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTCAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGACAC	AAGGTTTTTA	TCAGGTTGCC	1150
55	CATGGTACTA	GTGGATTGAC	AACTGGACGT	GCCTTTTCAA	ATGGTGCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAAATCG	CTGTCGCAGT	GGTCTTTTCT	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAC TAGAAA	GGAAATTA			1428

2) INFORMATION FOR SEQ ID NO: 1023

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

20	TGCCTCTATT	TCAAAGGAGA	TGCCTGGCAT	TAGTATTTCT	ACTTCTTGGG	50
	ATCGAAAGGT	TTTGGAAGCT	TCCCTTTCTT	CTATAGTAGG	GAGTGTATCC	100
	AGTGAAAAAG	CTGGTCTCCC	AGCGGAAGAA	GCAGAATCCT	ATCTTAAAAA	150
	AGGCTATTCT	CTAAATGACC	GTGTTGGAAC	CTCCTATTTG	GAAAAGCAAT	200
	ATGAAGAGAC	CTTACAAGGA	AAACGCTCGG	TAAAAGAAAT	CCATCTGGAT	250
25	AAATATGGCA	ATATGGAAAG	CGTGGACACA	ATTGAGGAAG	GTAAGTAAAGG	300
	AAACAATATC	AAACTGACCA	TTGATTTGGC	CTTCCAAGAT	AGCGTGGATG	350
	CTTTGCTGAA	AAGTTATTTT	AATTCGGAGC	TAGGAAATGG	TGGAGCTAAA	400
	TATTCTGAAG	GTGTCTATGC	AGTCGCCCTT	AACCCAAAAA	CAGGTGCTGT	450
	TTTATCCATG	TCAGGGATCA	AACATGACCT	GAAAACGGGA	GAGTTGACTC	500
30	CTGATTCCTT	GGGAACGGTA	ACCAATGTCT	TTGTCCCAGG	TTCGGTTGTC	550
	AAGGCTGCGA	CCATCAGCTC	AGGTTGGGAA	AATGGTGTTT	TATCAGGAAA	600
	CCAAACCTTA	ACAGATCAGC	CTATTGTTTT	CCAAGGTTCA	GCTCCAATTT	650
	ATTCTTG GTA	TAAATTGGCA	TATGGATCTT	TTCTATTAC	AGCTGTGGAA	700
	GCCTTGAGT	ATTCATCCAA	TGCTTACATG	GTTCAAACCG	CTCTTGGAAT	750
35	CATGGGCCAG	ACCTATCAAC	CAAATATGTT	TGTTGGAACC	AGCAATTGTT	800
	AAACAGCTAT	GGGAAAACCT	CGTGCAGACCT	TTGGCGAATA	TGGCTTGGGG	850
	GCTGCGACCG	GAATTGACCT	ACCAGATGAA	TCTACTGGAT	TTGTTCCCAA	900
	AGAGTATAGC	TTTGCTAATT	ACATCACCAA	TTCTTTTGGG	CAGTTTGATA	950
	ACTATACGCC	CATGCAGTTG	GCTCAGTATG	TAGCAACTAT	TGCAAATAAT	1000
40	GGTGTTCGTG	TGGCTCCTCG	TATTGTTGAA	GGCATTTATG	GTAATAATGA	1050
	TAAGGGAGGA	CTGGGTGACT	TGATTCAGCA	ACTGCAACCG	ACAGAGATGA	1100
	ATAAGGTCAA	TATATCCGAC	TCCGATATGA	GCATCTTGCA	CCAAGGTTTT	1150
	TATCAGGTTG	CCCATGGTAC	TAGTGGATTG	ACAACCTGGAC	GTGCCTTTTC	1200
	AAATGGTGCC	TTGGTATCCA	TTAGCGGAAA	AACAGGTACA	GCCGAAAGCT	1250
45	ATGTGGCAGA	TGGTCAGCAA	GCAACCAATA	CCAATGCGGT	GGCCTATGCC	1300
	CCATCTGATA	ATCCCCAAAT	CGCTGTGCGA	GTGGTCTTTC	CTCATAATAC	1350
	CAATCTAACA	AATGGTGTAG	GACCTTCCAT	TGCGCGTGAC	ATTATCAATC	1400
	TGTATCAAAA	ATACCATCCA	ATGAACTAGA	AAGGAAATTA	TG	1442

2) INFORMATION FOR SEQ ID NO: 1024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTTC	TACTTCTTGG	50
	GATCGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCTAA	400
	ATATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCTG	450
	TTTTATCCAT	GTCAGGGATC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTGCGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGTGTT	TTATCAGGAA	600
20	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAACT	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGAGTATAG	CTTTGCTAAT	TACATCACCA	ATTCCTTTGG	GCAGTTTGAT	950
	AACATATACAC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAATAAA	1000
	TGGTGTTTCGT	GTGGCTCCTC	GTATTGTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTGAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGCATCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCCCATGGTA	CTAGTGGATT	GACAACTGGA	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACAGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGCA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AATGAAGTAG	AAAGGAAATT	ATGCT	1445

2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTTC	TACTTCTTGG	50
	GATCGAAAGA	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCGTATTT	GGAAAAGCAA	200
60	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250

	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGTG	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAACT	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTCCCA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCCTTGG	GCAGTTTGAT	950
15	AACATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAAATGA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTCAGC	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCCT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACTGTTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	GTGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
25	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441

2) INFORMATION FOR SEQ ID NO: 1026

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCCGTT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
60	TGGAACAGC	TATGGGAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTA	1443

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2) INFORMATION FOR SEQ ID NO: 1027

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1443 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGTAGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAAACATGA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTTCTGTT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCCGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTCTGG	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
50	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACCTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCTCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	GACTTCTTAC	CTGGAAAAAC	200
	AATACGAGGA	AACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAGTATTCTG	AAGGCGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGACTTGA	500
30	CGCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGGTCAGTA	550
	GTTAAGGCCG	CTACCATCAG	CTCAGCTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	TAATGCCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGC	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
45	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTT	GCAGTGGTCT	TTCTCATATA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGC	1446

2) INFORMATION FOR SEQ ID NO: 1029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATAGAAAGG	TTTTTGAAAC	TTCCTTTTCT	TCTATAGTTG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAAGCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTAGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGATAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACCTGACC	ATTGATTGCG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTACTGA	AAAGTTATTT	CAATTCTGAG	CTAGAAAATG	GTGGAGCCAA	400
	GTATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCGG	450
	TTTTGTCTAT	GTCAGGGATT	AAACATGACT	TGAAAACGGG	AGAGTTGACG	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTTCCAG	GTTCGGTTGT	550
	CAAGGCGGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGAGTC	TTGTCAGGAA	600
20	ACCAGACCTT	GACAGACCAG	TCCATTGTCT	TCCAAGGTTT	AGCTCCCATC	650
	AATTCTTGGT	ATACTCAGGC	TTACGGTTCA	TTCCCTATCA	CAGCGGTCCA	700
	AGCTCTGGAG	TATTCATCCA	ATGCTTATAT	GGTCCAAACA	GCCTTAGGTC	750
	TTATGGGGCA	GACCTATCAA	CCCAATATGT	TTGTCGGCAC	CAGCAATCTA	800
	GAGTCTGCTA	TGGGTAAATT	GCGTTCAACC	TTTGCGGAAT	ATGGCTTGGG	850
25	GGCTGCGACT	GGGATTGATC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAA	CTTTGCCAAT	TTCATTACCA	ATGCCTTTTG	GCAGTTTGAT	950
	AACTATACCC	CAATGCAATT	GGCTCAGTAT	GTAGCAACTA	TTGCAAAATG	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTCAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTGTCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCTCATGGGA	CTAGTGGGTT	GACAACCTGC	CGTGCCTTTT	1200
	CAATAGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACGGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGGA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AAT			1423

40 2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1447 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

55	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
60	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250

	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCCGGT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCGAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
25	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGCT	1447

2) INFORMATION FOR SEQ ID NO: 1031

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCTTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTGGAA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAAC TATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GA CTGGGTGA	CTTGATTCAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACA ACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGA ACTA	GAAAGGAAAT	TATGCT	1446

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2) INFORMATION FOR SEQ ID NO: 1032

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1446 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAG	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGCTATT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACGAGCCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTCATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTGCGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAAC TATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATTCAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACA ACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGA	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCGTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAGCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCC	400
	AAGTATTCTG	AGGGTGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
30	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCTCATGG	GACTAGTGGA	TTGACAACTG	GACGTGCTTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGTGG	GAAAACAGGT	ACTGCCGAAA	1250
45	GTTATGTTGC	AGGTGGTCAA	GAAGCCAACA	ATACCAACGC	GGTGGCCTAT	1300
	GCCCCATCAG	ATAATCCTCA	AATCGCTGTT	GCCGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TTGGACCTTC	TATTGCACGC	GATATTATCA	1400
	ACCTCTATAA	CCAACACCAT	CCAATGAATT	AGAAAGGAAC	TTATGC	1446

2) INFORMATION FOR SEQ ID NO: 1034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-01

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

	GGAAACTGCA	GAGGTCAAGG	GGATTGATTT	TACAACCAGT	CCCAATCGTA	50
	GTTATCCAAA	CGGACAATTT	GCTTCTAGTT	TTATCGGACT	AGCTCAGCTC	100
10	CATGAAAATG	AAGATGGCAG	CAAGAGCTTA	CTGGGAACCT	CTGGAATGGA	150
	GAGTTCCTTG	AACAGTATTC	TTGCAGGGAC	AGACGGTATT	ATTACCTATG	200
	AAAAAGACCG	TGTAGGAAAT	ATCGTACCAG	GTACAGAACT	GGTATCGCAA	250
	CAAACCTGTG	ATGGCAAGGA	TGTTTATACA	ACATTGTCTA	GTCCGCTACA	300
	ATCTTTCATG	GAAACTCAGA	TGGATGCCTT	TCTAGAAAAA	GTAAAAGGTA	350
15	AGTATATGAC	CGCGACCTTG	GTCAGTGCAA	AGACCGGTGA	AATCCTCGCT	400
	ACCACCCAAC	GACCTACCTT	TAATGCAGAT	ACTAAAGAAG	GAATCACTGA	450
	GGACTTTTGT	TGGCGTGATA	TTCTTTTATCA	AAGTAACTAT	GAACCAGGAT	500
	CAGCCATGAA	GGTTATGACG	TTAGCTTCTT	CTATTGATAA	TAATACCTTC	550
	CCAAGTGGAG	AATACTTCAA	TAGCAGTGAA	TTCAAAATAG	CGGATGCGAC	600
20	GACTCGAGAT	TGGGATGTTA	ATGATGGTTT	GACTACTGGT	GGGATGATGA	650
	CTTTCTTACA	AGGTTTCGCT	CACTCCAGTA	ATGTTGGAAT	GAGTCTACTT	700
	GAACAAAAAA	TGGGAGATGC	TACTTG GTTG	GATTATCTAA	AACGCTTTAA	750
	ATTTGGGGTT	CCAACCTCGCT	TTGGCTTGAC	AGATGAATAC	GCTGGTCAAC	800
	TTCCAGCTGA	TAATATTGTT	AGTATTGCTC	AAAGCTCATT	TGGGCAAGGA	850
25	ATTTCACTGA	CACAAACACA	AATGCTTCGT	GCCTTTACAG	CTATTGCTAA	900
	TGATGGAGTT	ATGCTGGAGC	CAAAATTTAT	AAGTGCTATT	TATGATACTA	950
	ACAATCAGTC	TGTACGTAAG	TCACAAAAG	AAATAGTAGG	AAATCCTGTT	1000
	TCCAAAGAGG	CAGCAAGCAC	AACTCGAAAT	CACATGATCT	TAGTTGGGAC	1050
	GGACCCTCTA	TATGGAACATA	TGTATAATCA	CTACACAGGA	AAGCCAATTA	1100
30	TAACAGTTCC	TGGACAAAAT	GTAGCAGTTA	AATCCGGTAC	GGCTCAAATC	1150
	GCTGATGAGA	AAAATGGAGG	ATACTTGGTT	GGTTCTACCA	ATTATATTTT	1200
	CTCAGTTGTG	ACTATGAATC	CTGCTGAAAA	TCCTGATTTT	ATCTTGTATG	1250
	TAACGGTTCA	ACAGCCTGAG	CATTATTCAG	GTATCCAGTT	GGGAGAATTT	1300
	GCCACCCCAA	TCTTGGAGCG	GGCTTCAGCT	ATGAAAGAAT	CTCTCAATCT	1350
35	TCAATCTCCA	GCCAAAATTT	TAGATAAAGT	TACGACAGAA	TCTTCTTATG	1400
	CAATGCCTAG	CATCAAGGAT	ATTTACCTTG	GTGAGTTGGC	GGAAGCCTTA	1450
	CGCCGAAATA	TTGTGCAACC	AATCGTTGTA	GGTACTGGAA	CAAAGATTAA	1500
	AGAGACTTCT	GTAGAAGAAG	GGACCAATCT	TGCACCAAAC	CAACAAGTTC	1550
	TCCTTTTATC	GGATAAGGTA	GAAGAAATTC	CAGACATGTA	TGGCTGGAAA	1600
40	AAAGAGACTG	CCGAGACCTT	TGCTAAATGG	TTGGATATTG	AACTGGAATT	1650
	TGAAGGTTCA	GGTTCCGTTG				1670

45 2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1683 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

60

	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTTGC	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCTTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCCAGC	300
	CCCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	GTAAGTATGA	500
	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTTG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
35	CTGGAATTTG	AAGGTTCAGG	TTCCGTTGTT	CAG		1683

2) INFORMATION FOR SEQ ID NO: 1036

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-03
- 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTTATCGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTGCAGG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AAATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAAACTC	AGATGGATGC	CTTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAAACGCTT	TAAATTTGGG	GTTCCAACCTC	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACTTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCAG	TGACACAAAC	ACAAATGCTT	CGTGCCTTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCCT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TTAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGT	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TCTTCAATCT	CCAGCCAAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATGCAATGCC	TAGCATCAAG	GATATTTTAC	CTGGTGAGTT	1450
	GGCGGAAGCC	TTACGCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGCACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAACTGGA	ATTTGAAGGT	TCAGGTTCCG	TT		1682

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2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1681 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAGGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGGTTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACGAAC	250
45	TGGTATCGCA	ACAAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TAAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTTCAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

	TTAGTTGGGA	CGGACCCTCT	ATATGGAACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
5	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACACT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
10	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAAC TGGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCA		1685

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2) INFORMATION FOR SEQ ID NO: 1039

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1679 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

	AAAAGAATTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGACTA	100
35	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTAC	TGGGAACCTC	150
	TGGAATGGAG	AGTTCCCTTG	ACAGTATTCT	TGCAGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
40	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATTACTCAAT	AGCAGTGAAT	TCAAAATAGC	600
45	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGATGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
50	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
55	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGTTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
60	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400

CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550
AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
5 GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
ACTGGAATTT	GAAGGTTTCAG	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTTGA	AGGAATTGAC	TTCACAACCTA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTATTGGGT	100
	TTGGCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAAGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTGTTGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCCTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTCAAC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAAGTGGAA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

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2) INFORMATION FOR SEQ ID NO: 1041

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

20	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
	CAACCAGTCC	CAATCGTAGT	TATCCAAACG	GACAATTTGC	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGCTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCTTGAA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTA ACTATGA	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTTGGGACGG	ACCCTCTATA	TGGA ACTATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGATGTGA	ACGGTTC AAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTT CAGG	TTCCGTTGTT	CAGAAG	1696

2) INFORMATION FOR SEQ ID NO: 1042

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-09

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTA	GATGGCAAGG	ATGTTTATAC	GACTATTTC	300
	AGCACCTTC	AGTCCTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TAAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCCTTAC	AAGGTTTCGC	TCCTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCAAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATC	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCTTAT	CCTATGCCTA	GTGTCAAGGA	TATTTACCT	GGTGATTTAG	1450
	CAGAAGAATT	GCGTCGCAAT	CTTGTAACAAC	CCATCGTTGT	GGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAACCTGAAT	TTCAAGGTTC	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

60

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

5	CAAAAAAGAG	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCTAATCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGT	100
	CTAGCTCAAC	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
	TTATTACTTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
10	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTC	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAG	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
15	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
20	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
25	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGTACTTGGA	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
30	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
35	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	TGTTCAAGAAG		1690

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2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

	AGTTGGAAAC	TGCAGAGGTC	AAGGGGATTG	ATTTTACAAC	CAGTCCTAAT	50
	CGTAGTTACC	CAAACGGACA	ATTGCTTCT	AGTTTTATCG	GACTAGCTCA	100
60	GCTCCATGAA	AATGAAGATG	GCAGCAAGAG	CTTGCTGGGA	ACCTCTGGGA	150

	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCAG	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGGAACGG	AACAAGTTTC	250
	CCAACAAACG	GTAGATGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCAGT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTCT	AGATTGGGAT	GTTAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTC	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAACTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAACCT	TTCCTGGGCA	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGGC	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAACGG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAT	TTCTGTAGAA	GAAGGGACCA	ATCTTGACAC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTC	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTG	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	CTTAGTTGGG	1050
	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATGCCT	AGCATCAAGG	ATATTTCAAC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GTTTGGATAT	TGAACTGGAA	1650
	TTTGAAGGTT	CAGGTTCCTG	TGTTCAAGAAG			1680
25						

2) INFORMATION FOR SEQ ID NO: 1046

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTATATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTGC	TTTGGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAAT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAAGTGAAT	TTGAAGGTTT	AGGTTCCGTT	GTTTACAAG		1689

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2) INFORMATION FOR SEQ ID NO: 1047

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTT	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGCGGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCCTATG	AAAGTGTATG	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAAATGAT	GACCTTTTCT	CAAGGGTTTC	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
	TTTGGACAAG	GGATTTCAGC	GACCCAGACG	CAATGATTC	GTGCCTTCAC	900
55	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCCGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAACGTG	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGA	AGGGCAGTGG	CTATGAAAGA	1350
	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAAC	GTTAAATCAG	GTAACCAATC	1400
5	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTCACC	TGGCGATTTG	1450
	GCGGAAGCCT	TACGTCGCAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGCACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTF	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTGGA	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550

AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
GGCTGGAAAA	AAGAGACTGC	TGAAACCTTT	GCTAAATGGT	TGGATATTGA	1650
GTTGGAATTT	GAAGGTTTCA	GTTCCGTCGT	TC		1682

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2) INFORMATION FOR SEQ ID NO: 1049

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1241 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R690

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

GCAGCGTTGC	GTGATACCGT	TGAAAAAACC	ATTAAAAACT	GTTTGGATTT	50
TGAAAGGAGA	CAGGAGCATG	AATAGAATAA	AAGTTGCAAT	ACTGTTTGGG	100
GGTTGCTCAG	AGGAGCATGA	CGTATCGGTA	AAATCTGCAA	TAGAGATAGC	150
CGCTAACATT	AATAAAGAAA	AATACGAGCC	GTTATACATT	GGAATTACGA	200
AATCTGGTGT	ATGGAAAATG	TGCGAAAAAC	CTTGCGCGGA	ATGGGAAAAC	250
GACAATTGCT	ATTCAGCTGT	ACTCTCGCCG	GATAAAAAAA	TGCACGGATT	300
ACTTGTTAAA	AAGAACCATG	AATATGAAAT	CAACCATGTT	GATGTAGCAT	350
TTTCAGCTTT	GCATGGCAAG	TCAGGTGAAG	ATGGATCCAT	ACAAGGTCTG	400
TTTGAATTGT	CCGGTATCCC	TTTTGTAGGC	TGCGATATTC	AAAGCTCAGC	450
AATTTGTATG	GACAAATCGT	TGACATACAT	CGTTGCGAAA	AATGCTGGGA	500
TAGCTACTCC	CGCCTTTTGG	GTTATTAATA	AAGATGATAG	GCCGGTGGCA	550
GCTACGTTTA	CCTATCCTGT	TTTTGTTAAG	CCGGCGCGTT	CAGGCTCATC	600
CTTCGGTGTG	AAAAAAGTCA	ATAGCGCGGA	CGAATTGGAC	TACGCAATTG	650
AATCGGCAAG	ACAATATGAC	AGCAAAATCT	TAATTGAGCA	GGCTGTTTCG	700
GGCTGTGAGG	TCGGTTGTGC	GGTATTGGGA	AACAGTGCCG	CGTTAGCTGT	750
TGGCGAGGTG	GACCAAATCA	GGCTGCAGTA	CGGAATCTTT	CGTATTCATC	800
AGGAAGTCGA	GCCGGAAAAA	GGCTCTGAAA	ACGCAGTTAT	AACCGTTCCC	850
GCAGACCTTT	CAGCAGAGGA	GCGAGGACGG	ATACAGGAAA	CGGCAAAAAA	900
AATATATAAA	GCGCTCGGCT	GTAGAGGTCT	AGCCCGTGTG	GATATGTTTT	950
TACAAGATAA	CGGCCGCATT	GTAAGTGAACG	AAGTCAATAC	TCTGCCCGGT	1000
TTCACGTCAT	ACAGTCGTTA	TCCCCGTATG	ATGGCCGCTG	CAGGTATTGC	1050
ACTTCCCGAA	CTGATTGACC	GCTTGATCTG	ATTAGCGTTA	AAGGGGTGAT	1100
AAGCATGGAA	ATAGGATTTA	CTTTTTTAGA	TGAAATAGTA	CACGGTGTTC	1150
GTTGGGACGC	TAAATATGCC	ACTTGGGATA	ATTTACCCGG	AAAACCGGTT	1200
GACGGTTATG	AAGTAAATCG	CATTGTAGGG	ACATACGAAT	T	1241

50

2) INFORMATION FOR SEQ ID NO: 1050

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1249 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
10	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
15	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
20	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
25	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
30	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCG	1249

35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

50	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAAACTG	50
	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	100
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	150
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	200
55	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	250
	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	300
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	350
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	400
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	450
60	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	500

	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	550
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	600
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	650
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	700
5	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	750
	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	800
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	850
	ACCGTTCCCC	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	900
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	950
10	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1000
	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1050
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1100
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTAGAT	GAAATAGTAC	1150
	ACCGTGTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1200
15	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAATT	1250
	GGCTTGAATC	GCTTTTTGAA	GG			1272

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

35	TCCCCCGGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGAATTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
40	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
45	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
50	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCC	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
55	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	1200
60	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTA		1237

2) INFORMATION FOR SEQ ID NO: 1053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

20	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	TTGAAAAAAC	50
	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	GAATAGAATA	100
	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	ACGTATCGGT	150
	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	AAATACGAGC	200
	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	GTGCGAAAAA	250
25	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	TACTCTCGCC	300
	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	GAATATGAAA	350
	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	GTCAGGTGAA	400
	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	CTTTTGTAGG	450
	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	TTGACATACA	500
30	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	GGTTATTAAT	550
	AAAGATGATA	GGCCGGTGCG	AGCTACGTTT	ACCTATCCTG	TTTTTGTTAA	600
	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	AATAGCGCGG	650
	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	CAGCAAAATC	700
	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	CGGTATTGGG	750
35	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	AGGCTGCAGT	800
	ACGGAATCTT	TCGTATTTCAT	CAGGAAGTCG	AGCCGGAAAA	AGGCTCTGAA	850
	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	AGCGAGGACG	900
	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	TGTAGAGGTC	950
	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	TGTACTGAAC	1000
40	GAAGTCAATA	CTCTGCCCGG	TTTCACGTCA	TACAGTCGTT	ATCCCCGTAT	1050
	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	CGCTTGATCG	1100
	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	ACTTTTTTTAG	1150
	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	CACTTGGGAT	1200
	AATTTACCGG	GAAAACCGGT	TGACGGGTAT	GAAAGTAAAT	CGCATTGTAG	1250
45	GGACATTCGA	ATT				1263

2) INFORMATION FOR SEQ ID NO: 1054

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

5	CGGCCTATTA	TNCCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	50
	AAAAACTGTT	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAAG	100
	TTGCAATACT	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	150
	TCTGCAATAG	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	200
	ATACATTGGA	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	250
10	GCGCGGAATG	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	300
	AAAAAAATGC	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	350
	CCATGTTGAT	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	400
	GATCCATACA	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	450
	GATATTCAAA	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	500
15	TGCGAAAAAT	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	550
	ATGATAGGCC	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	600
	GCGCGTTCAG	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	650
	ATTGGACTAC	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	700
	TTGAGCAGGC	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	750
20	AGTGCCGCGT	TAGTTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	800
	AATCTTTCGT	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	850
	CAGTTATAAC	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	900
	CAGGAAACGG	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	950
	CCGTGTGGAT	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	1000
25	TCAATACTCT	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	1050
	GCCGCTGCAG	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	1100
	AGCGTTAAAG	GGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	1150
	AATAGTACAC	GGTGTTTCGT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	1200
	TCACCGGAAA	ACCGGTTGAC	GGTTATAAGT	AA		1232
30						

2) INFORMATION FOR SEQ ID NO: 1055

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1218 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
40	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Enterococcus gallinarum</i>
45	(B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

	TACCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	AAAAACTGTT	50
50	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAAG	TTGCAATACT	100
	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	TCTGCAATAG	150
	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	ATACATTGGA	200
	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	GCGCGGAATG	250
	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	AAAAAAATGC	300
55	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	CCATGTTGAT	350
	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	GATCCATACA	400
	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	GATATTCAAA	450
	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	TGCGAAAAAT	500
	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	ATGATAGGCC	550
60	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	GCGCGTTCAG	600

	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTtagatga	AATAGTACAC	1150
	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTtagaa				1218

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2) INFORMATION FOR SEQ ID NO: 1056

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R688

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	150
	ACGTATCGGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGGC	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTGTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTTCAT	CAGGAAGTCG	AGCCGGAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCCG	TTTCACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTAG	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTACCCG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

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2) INFORMATION FOR SEQ ID NO: 1057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
20	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
25	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
30	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTTCG	GCTGTGAGGT	CGGTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
35	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
40	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
	ATTGTAGGGA	CATACGAAT				1269

2) INFORMATION FOR SEQ ID NO: 1058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAAAC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTTCGTCAC	950
	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1166 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTCGTCAC	950
5	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTG				1166

10

2) INFORMATION FOR SEQ ID NO: 1060

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

	AACATGAAAA	AAATCGCCTT	ATTTTTGGAG	GCAATTCACC	GGAATACACC	50
30	GTTTCTTTAG	CTTCAGCAAC	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	100
	CTATGACTAC	GACCTCTCTT	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	150
	GGTACTTGTA	TACAGGAGAA	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	200
	TTGGATACGA	AACATAAACA	GAAAATACAG	CCGCTATTCT	AAGGAAACGG	250
	CTTTTGGCTA	AGTGAAGAGC	AGCAAACGTT	GGTACCTGAT	GTTTTATTTT	300
35	CCATTATGCA	TGGCAAATAC	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	350
	GAATTGATGA	AGCTGCCTTA	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	400
	ATGTATGAAC	AAATGGCTGC	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	450
	AAAGTGCTCC	TACGATTCTC	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	500
	ATCGAAGCTT	TTATCCAGAC	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	550
40	TGAAGCGGGC	TCCTCAAAAG	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	600
	TCGCTTCTGC	CTTAAAAGAA	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	650
	CAAAAAAATA	TTGCCGGTGT	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	700
	CTCTTTGACT	GTCGGTGCTT	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	750
	TCGATTTTGA	AGAAAAGTAC	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	800
45	GCGCCATTGC	CTGAAACGAT	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	850
	GCTCTATCGT	AGTCTTGGTC	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	900
	TCACGGAGCG	AGGAGAACTA	TACTTGAATG	AAATCAATAC	TATGCCGGGC	950
	TTTACGAGTC	ACTCCCGCTA	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	1000
	CTATCAAGAA	CTACTACAAA	AACTGCTT			1028

50

2) INFORMATION FOR SEQ ID NO: 1061

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

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10  AATATGAAAA AAATCGCCTT ATTTTTGGAG GCAATTCACC GGAGTACGCC      50
    GTTTCCTTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
    CGATGACTAT  GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
    GGTATTTGTA  TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
    TTGGATACGA AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
    CTTTTGGCTA AGTGAAGAGC AACAAACGTT GGTTCCTGAT GTTTTATTTT      300
15  CCATTATGCA  TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
    GAATTGATGA AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
    ATGTATGAAC AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
    AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
    ATCGAAGCTT TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20  TGAAGCGGGC TCCTCAAAGG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
    TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTTCAGC AGTGCTCCTA      650
    CAAAAAATA  TTGCCGGTGT TGAGATCGGT TCGGGTATTT TGGGCAACGA      700
    CTCTTTGACT GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
    TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25  GCACCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
    GCTCTATCGT AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTG      900
    TCACGGATCA AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
    TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
30  CTATCAAGAA CTACTACAAA AACTGCTTGT      1030

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2) INFORMATION FOR SEQ ID NO: 1062

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1031 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

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50  AAACATGAAA AAAATCGCCA TTATTTTTGG AGGCAATTCA CCGGAATACA      50
    CCGTTTTCTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
    CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
    TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
    TGTGATGATG GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
    GGCTTTTGGC TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
55  TCCCATATAT CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
    TTGAATTGAT GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
    TTATGTATGA ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
    ACAAAGTGCT CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
    AAATCGAAGC TTTTATCCAG ACCCATGGCT TCCAGTTTCT CTTTAAGCCT      550
60  AATGAAGCGG GCTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

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	AATCGCTTCT	GCCTTAAAAG	AAGCCTTTAC	TTATTGTTCC	GCAGTGCTCC	650
	TACAAAAAAA	TATTGCCGGT	GTTGAGATCG	GTTGCGGTAT	TTTGGGCAAC	700
	GACTCTTTGA	CTGTCGGTGC	TTGTGACGCC	ATTTCATTAG	TAGACGGCTT	750
	TTTCGATTTT	GAAGAAAAGT	ACCAGCTGAT	CAGCGCCAAA	ATCACCGTCC	800
5	CTGCGCCATT	GCCTGAAACG	ATTGAAACCA	AGGTCAAAGA	ACAAGCTCAG	850
	CTGCTCTATC	GTAGTCTTGG	TCTTAAAGGT	CTTGCTCGCA	TCGACTTTTT	900
	TGTCACGGAG	CGAGGAGAAC	TATACTTGAA	TGAAATCAAT	ACTATGCCGG	950
	GCTTTACGAG	TCACTCCCGC	TATCCTGCCA	TGATGGCAGC	GGTCGGCTTA	1000
	TCCTATCAAG	AACTACTACA	AAAAGTCTT	G		1031

10

2) INFORMATION FOR SEQ ID NO: 1063

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R775

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

	AACATGAAAA	AAATCGCCAT	TATTTTTTGA	GGCAATTCAC	CGGAATACAC	50
30	CGTTTCTTTA	GCTTCAGCAA	CTAGCGCAAT	CGAAGCACTC	CAATCATCTC	100
	CCTATGACTA	CGACCTCTCT	TTGATCGGGA	TCGCCCCAGA	TGCTATGGAT	150
	TGGTACTTGT	ATACAGGAGA	ACTGGAAAAC	ATCCGACAAG	ACACGTGGTT	200
	GTTGGATACG	AAACATAAAC	AGAAAATACA	GCCGCTATTT	GAAGGAAACG	250
	GCTTTTGGCT	AAGTGAAGAG	CAGCAAACGT	TAGTACCTGA	TATTTTATTT	300
35	CCCATTATGC	ATGGCAAATA	CGGGGAAGAT	GGCAGTATCC	AAGGATTGTT	350
	TGAATTGATG	AAACTACCTT	ATGTAGGTTG	CGGGGTGGCA	GGTTCCTGCCT	400
	TATGTATGAA	CAAATGGCTG	CTGCATCAAG	CTGCAGCAGC	CATTGGCGTA	450
	CAAAGTGCTC	CTACGATTCT	CTTGACAAAT	CAAGCCAACC	AGCAAGAACA	500
	AATCGAAGCT	TTTATCCAGA	CCCATGGCTT	CCCAGTTTTT	TTTAAGCCTA	550
40	ATGAAGCGGG	CTCTTCAAAA	GGGATCACTA	AAGTCACCTG	CGTTGAAGAA	600
	ATCGCTTCTG	CCTTAAAAAA	AGCCTTTACT	TATTGTTCCG	CAGTGCTCCT	650
	ACAAAAAAAT	ATTGCCGGTG	TTGAGATCGG	TTGCGGTATT	TTGGGCAACG	700
	ACTCTTTGAC	TGTCGGTGCT	TGTGACGCCA	TTTCATTAGT	AGACGGCTTT	750
	TTCGATTTTG	AAGAAAAGTA	CCAGCTGATC	AGCGCCAAAA	TCACCGTCCC	800
45	TGCGCCATTG	CCTGAAACGA	TTGAAACCAA	GGTCAAAGAA	CAAGCTCAGC	850
	TGCTCTATCG	TAGTCTTGGT	CTTAAAGGTC	TTGCTCGCAT	CGACTTTTTT	900
	GTCACGGATC	AAGGAGAACT	ATACTTGAAT	GAAATCAATA	CTATGCCGGG	950
	CTTTACGAGT	CACTCCCGTT	ATCCTGCCAT	GATGGCAGCG	GTCGGCTTAT	1000
	CCTATCAAGA	ACTACTACAA	AAAGTCTTG			1030

50

2) INFORMATION FOR SEQ ID NO: 1064

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

5 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

	AAACATGAAA	AAAATCGCCA	TTATTTTTTG	AGGCAATTCA	CCGGAATACA	50
10	CCGTTTCTTT	AGCTTCAGCA	ACTAGCGCAA	TGAAGCACT	CCAATCATCT	100
	CCCTATGACT	ACGACCTCTC	TTTGATCGGG	ATCGCCCCAG	ATGCTATGGA	150
	TTGGTACTTG	TATACAGGAG	AACTGGAAAA	CATCCGACAA	GACACGTGGT	200
	TGTTGGATAC	GAAACAGAAA	CAGAAAATAC	AGCCGCTATT	CGAAGGAAAC	250
	GGCTTTTGGT	TAAGTGAAGA	GCAGCAAACG	TTGGTACCTG	ATGTTTTATT	300
15	TCCCATTATG	CATGGCAAAT	ACGGGGAAGA	TGGCAGTATC	CAAGGATTGT	350
	TTGAATTGAT	GAAGCTACCT	TATGTAGGCT	GCGGGGTGGC	AGGTCTTGCC	400
	TTATGTATGA	ACAAATGGTT	GCTGCATCAA	GCTGCAGCAG	CCATTGGCGT	450
	ACAAAGTGCT	CCTACGATTC	TCTTGACAAA	TCACGCCAAC	CAGCAAGAAC	500
	AAATCGAAGC	TTTTATCCAG	ACCCATGGCT	TTCCAGTTTT	CTTTAAGCCT	550
20	AATGAAGCGG	GTTCTCATA	AGGGATCACT	AAAGTCACCT	GCGTTGAAGA	600
	AATCGCTTCT	GCCTTAAAAG	AAGCCTTTAC	TTATTGTTCC	GCAGTGCTCC	650
	TACAAAAAAA	TATTGCCGGT	GTTGAGATCG	GTTGCGGTAT	TTTGGGCAAC	700
	GACTCTTTGA	CTGTCGGTGC	TTGTGACGCC	ATTTTCATTAG	TAGACGGCTT	750
	TTTCGATTTT	GAAGAAAAGT	ACCAGCTGAT	CAGCGCCAAA	ATCACCGTCC	800
25	CTGCGCCATT	GCCTGAAACG	ATTGAAACTA	AGGTCAAAGA	ACAAGCTCAG	850
	CTGCTCTATC	GTAGTCTTGG	ACTTAAAGGT	CTTGCTCGCA	TCGACTTTTT	900
	TGTCACGGAT	CAAGGAGAAC	TATACTTGAA	TGAAATCAAT	ACTATGCCGG	950
	GCTTTACGAG	TCACTCCCGC	TATCCTGCCA	TGATGGCAGC	GGTCGGGTTA	1000
30	TCCTATCAAG	AACTACTACA	AAAACACTTT	GT		1032

2) INFORMATION FOR SEQ ID NO: 1065

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

45 (B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

	AAAAACATGA	AAAAAATCGC	CATTATTTTT	GGAGGCAATT	CACCGGAATA	50
50	CACCGTTTCT	TTAGCTTCAG	CAACTAGCGC	AATCGAAGCA	CTCCAATCAT	100
	CTCCCTATGA	CTACGACCTC	TCTTTGATCG	GGATCGCCCC	AGATGCTATG	150
	GATTGGTACT	TGTATACAGG	AGAACTGGAA	AACATCCGAC	AAGACACGTG	200
	GTTGTTGGAT	ACGAAACATA	AACAGAAAAT	ACAGCCGCTA	TTCGAAGGAA	250
	ACGGCTTTTG	GCTAAGTGAA	GAGCAGCAAA	CGTTGGTACC	TGATGTTTTA	300
55	TTTCCCATTA	TGCATGGCAA	ATACGGGGAA	GATGGCAGTA	TCCAAGGATT	350
	GTTTGAATTG	ATGAAGCTGC	CTTATGTAGG	CTGCGGGGTG	GCAAGTTCTG	400
	CCTTATGTAT	GAACAAATGG	CTGCTGCATC	AAGCTGCAGC	AGCCATTGGC	450
	GTACAAAGTG	CTCCTACGAT	TCTCTTGACA	AATCAAGCCA	ACCAGCAAGA	500
	ACAAATCGAA	GCTTTTATCC	AGACCCATGG	CTTTCAGTT	TTCTTTAAGC	550
60	CTAATGAAGC	GGGCTCCTCA	AAAGGGATCA	CTAAAGTCAC	CTGCGTTGAA	600

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1000 GAAATCGCTT CTGCCTTAAA AGAAGCCTTT ACTTATTGTT CCGCAGTGCT 650
      CCTACAAAAA AATATTGCCG GTGTTGAGAT CGGTTGCGGT ATTTTGGGCA 700
      ACGACTCTTT GACTGTCCGGT GCTTGTGACG CCATTTCATT AGTAGACGGC 750
      TTTTTCGATT TTGAAGAAAA GTACCAGCTG ATCAGCGCCA AAATCACCGT 800
5     CCCTGCGCCA TTGCCTGAAA CGATTGAAAC CAAGGTCAAA GAACAAGCTC 850
      AGCTGCTCTA TCGTAGTCTT GGTCTTAAAG GTCTTGCTCG CATCGACTTT 900
      TTTGTCACGG ATCAAGGAGA ACTATACTTG AATGAAATCA ATACTATGCC 950
      GGGCTTTACG AGTCACTCCC GCTATCCTGC CATGATGGCA GCGGTCGGCT 1000
      TATCCTATCA AGAACTACTA CAAAACTGC TTGT 1034
10

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2) INFORMATION FOR SEQ ID NO: 1066

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15     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1012 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Enterococcus flavescens
25     (B) STRAIN: R760

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

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30     CATGAAAAAA ATCGCCATTA TTTTGGAGG CAATTCACCG GAATACACCG 50
      TTTCTTTAGC CTCAGCAACT AGCGCAATCG AAGCACTCCA ATCATCTCCC 100
      TATGATTACG ACCTCTCTTT GATCGGGATC GCCCCAGATG CTATGGATTG 150
      GTACTTGTAT ACAGGAGAAC TGGAAAACAT CCGACAAGAC ACGTGGTTGT 200
      TGGATACGAA ACATACACAG AAAATCCAGC CACTTTTGA AGGAAACGGC 250
      TTTTGGATAA GTGAAGCGCA GCAAACGTTG GTACCTGATG TTTTATTTCC 300
35     CATTATGCAT GGTAAATACG GGAAGATGG CAGTATCCAA GGATTGTTTG 350
      AATTGATGAA GCTGCCTTAT GTAGGCTGTG GGGTGGCAGC CTCTGCCTTA 400
      TGTATGAACA AATGGTTATT GCATCAAGCA GCAGCAGCGA TTGGCGTACA 450
      AAGCGCTCCT ACGATTCTCT TGACAAATCA AGCCAACCAG CAAAGACAAA 500
      TCGAAGCCTT TATCCAGACC CATGGCTTTC CAGTTTTCTT TAAGCCTAAT 550
40     GAAGCGGGCT CCTCAAAGG GATCACAAA GTAACCTGTG TTGAAGAAAT 600
      CGCTCCTGCC TTGAAGGAAG CCTTCGCTTA TTGTTCCGCA GTGCTCTTAC 650
      AAAAAAATAT CGCTGGCGTT GAGATTGGTT GCGGTATCTT AGGCAACGAC 700
      TCTTTGACTG TCGGTGCTTG TGACGCTATT TCATTAGTAG ACGGCTTTTT 750
      CGATTTTGAA GAAAAGTACC AGTTGATCAG CGCCAAAATC ACCGTTCTTG 800
45     CGCCATTGCC TGAAACGATT GAAACCAAAG TCAAAGAACA AGCTCAGCTG 850
      CTCTATCACA GTCTTGGTCT TAAAGGACTT GCTCGCATCG ACTTTTTTGT 900
      CACGGATCAA GGAGAACTAT ACTTGAATGA AATCAATACT ATGCCGGGCT 950
      TTACGAGTCA CTCCCGCTAT CCTGCCATGA TGGCAGCGGT CGGCTTATCC 1000
      TATCAAGAAT TA 1012
50

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2) INFORMATION FOR SEQ ID NO: 1067

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55     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 721 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
60

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

10	CTTACGCTTT	ATCGATTAGA	CACGGGNAGC	TTGTCCAATG	GGRAGCCGAT	50
	TTGATTTTAT	GGATGAACGC	TCTCATCATG	CGGCAAATGG	AATATCATGC	100
	AATGAAGCGC	AAAATCGCAG	ACGTTTGCGC	TCCATCATGG	AAAACAGTGG	150
	TTTTGAAGCA	TATAGCCTCG	AATGGTGCCA	CTATGTATTA	AGAGACGAAC	200
	CATACCCCAA	TAGCTATTTT	GATTTCCCGG	TTAAATAAAC	TTTTAACCGT	250
	TGCACGGACA	AACTATATAA	GCTAACTCTT	TCGGCAGGAA	ACCCGACGTA	300
15	TGTAAGTGGT	TCTTAGGGAA	TTTATATATA	GTAAGATAGT	TTGAAGATGT	350
	AAGGCAGAGC	GATATTGCGG	TCATTATCTG	CGTGCGCTGC	GGCAAGATAG	400
	CCTGATAATA	AGACTGATCG	CATAGAGGGG	TGGTATTTCA	CACCGCCCAT	450
	TGTCAACAGG	CAGTTCAGCC	TCGTTAAATT	CAGCATGGGT	ATCACTTATG	500
	AAAATTCATC	TACATTGGTG	ATAATAGTAA	ATCCAGTAGG	GCGAAATAAT	550
20	TGACTGTAAT	TTACGGGGCA	AAACGGCACA	ATCTCAAACG	AGATTGTGCC	600
	GTTTAAGGGG	AAGATTCTAG	AAATATTTCA	TACTTCCAAC	TATATAGTTA	650
	AGGAGGAGAC	TGAAAATGAA	GAAGTTGTTT	TTTTTATTGT	TATTGTTATT	700
	CTTAATATAC	TTAGGTTATT	G			721

25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

45	ATTTTAAAGG	ATGAACGCTC	TTCATCATGC	GGCAAATGGA	ATATCATGCA	50
	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	CCATCATGGA	AAACAGTGGG	100
	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	TATGTATTAA	GAGACGAACC	150
	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	TAAATAAACT	TTTAACCGTT	200
	GCACGGACAA	ACTATATAAG	CTAACTCTTT	CGGCAGGAAA	CCCGACGTAT	250
	GTAAGTGGTT	CTTAGGGAAT	TTATATATAG	TAGATAGTAT	TGAAGATGTA	300
	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	GTGCGCTGCG	GCAAGATAGC	350
50	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	GGTATTTTAC	ACCGCCCAT	400
	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	AGCATGGGTA	TCACTTATGA	450
	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	TCCAGTAGGG	CGAAATAATT	500
	GACTGTAAAT	TACGGGGCAA	AACGGCACAA	TCTCAAACGA	GATTGTGCCG	550
	TTTAAGGGGA	AGATTCTAGA	AATATTTTCA	ACTTCCAAC	ATATAGTTAA	600
55	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	TTTTATTGTT	ATTGTTATTC	650
	TTAATATACT	TAGGTTAT				668

60 2) INFORMATION FOR SEQ ID NO: 1069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

```

15  CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT      50
    GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC      100
    GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT      150
    CCATCATGGA AAACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC      200
20  TATGTATTAA GAGACGAACC ATACCCAAT AGCTATTTTG ATTTCCCGT      250
    TAAATAAACT TTTAACCGTT GCACGGACAA ACTATATAAG CTAACCTCTT      300
    CGGCAGGAAA CCCGACGTAT GTAAC TGGTT CTTAGGGAAT TTATATATAG      350
    TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC      400
    GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT      450
25  GGTATTTTAC ACCGCCCAT TGTCAACAGGC AGTTCAGCCT CGTTAAATTC      500
    AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA      550
    TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA      600
    TCTCAAACGA GATTGTGCCG TTTAAGGGGA AGATTCTAGA AATATTTTAT      650
    ACTTCCAAC TATAGTTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT      700
30  TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTTAAT      750
    GAAANCCTGA                                     760
  
```

2) INFORMATION FOR SEQ ID NO: 1070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

```

50  AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT      50
    GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGTAAC      100
    AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC      150
    AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA      200
55  TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT      250
    GTATTAAGAG ACGAACCATA CCCCAATAGC TATTTTGATT TCCCCGTAA      300
    ATAACTTTT AACCGTTGCA CGGACAACT ATATAAGCTA ACTCTTTCGG      350
    CAGGAAACCC GACGTATGTA ACTGGTTCTT AGGGAATTGA TATATAGTAG      400
    ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG      450
60  CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT      500
  
```

```

ATTTCACACC GCCATTGTC AACAGGCAGT TCAGCCTCGT TAAATTCAGC 550
ATGGGTATCA CTTATGAAAA TTCATCTACA TTGGTGATAA TAGTAAATCC 600
AGTAGGGCGA AATAATTGAC TGTAATTTAC GGGGCAAAAC GGCACAATCT 650
CAAACGAGAT TGTGCCGTTT AAGGGGAAGA TTCTAGAAAT ATTTCATACT 700
5 TCCAACATA TAGTTAAGGA GGAGACTGAA AATGAAGAAG TTGTTTTTTT 750
TTATTGTTAT TGTATTCTT AATATACTTA GTTATGACT ACGTTAATGA 800
A 801

```

10

2) INFORMATION FOR SEQ ID NO: 1071

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 711 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R684

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

```

TTGTACCAAT GGGGAGCCGA TTTGATTTTA TGGATGAACG CTCTCATCAT 50
GCGGCAAATG GAATATCATG CAATGAAGCG CAAAATCGCA GACGTTTGCG 100
CTCCATCATG GAAAACAGTG GGTTTGAAGC ATATAGCCTC GAATGGTGGC 150
30 ACTATGTATT AAGAGACGAA CCATACCCCA ATAGCTATTT TGATTTCCCC 200
GTTAAATAAA CTTTTAACCG TTGCACGGAC AAACATATA AGCTAACTCT 250
TTCGGCAGGA AACCCGACGT ATGTAAGTGG TTCTTAGGGA ATTTATATAT 300
AGTAGATAGT ATTGAAGATG TAAGGCAGAG CGATATTGCG GTCATTATCT 350
GCGTGCGCTG CGGCAAGATA GCCTGATAAT AAGACTGATC GCATAGAGGG 400
35 GTGGTATTTT ACACCGCCCA TTGTCAACAG GCAGTTCAGC CTCGTTAAAT 450
TCAGCATGGG TATCACTTAT GAAAATTCAT CTACATTGGT GATAATAGTA 500
AATCCAGTAG GCGGAAATAA TTGACTGTAA TTTACGGGGC AAAACGGCAC 550
AATCTCAAAC GAGATTGTGC CGTTTAAGGG GAAGATTCTA GAAATATTTT 600
ATACTTCCAA CTATATAGTT AAGGAGGAGA CTGAAAATGA AGAAGTTGTT 650
40 TTTTTTATTG TTATTGTTAT TCTTAATATA CTTAGGTTAT GACTACGTTA 700
ATGAAGCACT G 711

```

45 2) INFORMATION FOR SEQ ID NO: 1072

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072

60

	GCCATTGATC	TTACGCTTTA	TCGATTAGAC	ACGGGTNAGC	TTGTACCAAT	50
	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	GCGGCAAATG	100
	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	CTCCATCATG	150
	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	ACTATGTATT	200
5	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	GTAAATAAAA	250
	CTTTTAACCG	TTGCACGGAC	AACTATATA	AGCTAACTCT	TTCGGCAGGA	300
	AACCCGACGT	ATGTAAGTGG	TTCTTAGGGA	ATTTATATAT	AGTAGATAGT	350
	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	GCGTGCGCTG	400
	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	GTGGTATTTT	450
10	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	TCAGCATGGG	500
	TATCACTTAT	GAAAATTCAT	CTACATTGGT	GATAATAGTA	AATCCAGTAG	550
	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	AATCTCAAAC	600
	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	ATACTTCCAA	650
	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	TTTTTTATTG	700
15	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	ATGAAGCACT	750
	G					751

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

35	ATTTGATTTT	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	50
	GCAATGAAGC	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	100
	GGGTTTGAAG	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	150
	ACCATACCCC	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	200
40	GTTGCACGGA	CAAACATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	250
	TATGTAAGT	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	300
	GTAAGGCAGA	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	350
	AGCCTGATAA	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	400
	ATTGTCAACA	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	450
45	TGAAAATTCA	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	500
	ATTGACTGTA	ATTTACGGGG	CAAAACGGCA	CAATCTCAA	CGAGATTGTG	550
	CCGTTTAAAG	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	600
	TAAGGAGGAG	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	650
50	TTCTTAATAT	ACTTAGGTTA	TGACTACGTT	AATGA		685

2) INFORMATION FOR SEQ ID NO: 1074

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

5 (B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

```

10 ATCGATTAGA CACGGGTGAG CTTGTACCAA TGGGGAGCCG ATTTGATTTT 50
   ATGGATGAAC GCTCTCATCA TGC GGCAAAT GGAATATCAT GCAATGAAGC 100
   GCAAAATCGC AGACGTTTGC GCTCCATCAT GGAAACAGT GGGTTTGAAG 150
   CATATAGCCT CGAATGGTGG CACTATGTAT TAAGAGACGA ACCATACCCC 200
   AATAGCTATT TTGATTTCCC CGTTAAATAA ACTTTTAACC GTTGCACGGA 250
   CAAACTATAT AAGCTAACTC TTTCGGCAGG AAACCCGACG TATGTAAC TG 300
15 GTTCTTAGGG AATTTATATA TAGTAGATAG TATTGAAGAT GTAAGGCAGA 350
   GCGATATTGC GGTCAATTATC TGC GTGCGCT GCGGCAAGAT AGCCTGATAA 400
   TAAGACTGAT CCGCATAGAG GGTGGTATTT CACACCGCCC ATTGTCAACA 450
   GGCAGTTCAG CCTCGTTAAA TTCAGCATGG GTATCACTTA TGAAAATTCA 500
   TCTACATTGG TGATAATAGT AAATCCAGTA GGGCGAAATA ATTGACTGTA 550
20 ATTTACGGGG CAAAACGGCA CAATCTCAA CGAGATTGTG CCGTTTAAGG 600
   GGAAGATTCT AGAAATATTT CATACTTCCA ACTATATAGT TAAGGAGGAG 650
   ACTGAAAATG AAGAAGTTGT TTTTTTTATT GTTATTGTTA TTCTTAATAT 700
   ACTTAGGTTA TGA CTACGTT AATGAAGCAC TG 732

```

25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

40 (B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

```

45 TCTCATCATG CGGCAAATGG AATATCATGC AATGAAGCGC AAAATCGCAG 50
   ACGTTTGC GC TCCATCATGG AAAACAGTGG GTTTGAAGCA TATAGCCTCG 100
   AATGGTGGCA CTATGTATTA AGAGACGAAC CATACCCCAA TAGCTATTTT 150
   GATTTCCCCG TTAAATAAAC TTTTAACCGT TGCACGGACA AACTATATAA 200
   GCTAACTCTT TCGGCAGGAA ACCCGACGTA TGTAAGTGGT TCTTAGGGAA 250
   TTTATATATA GTAGATAGTA TTGAAGATGT AAGGCAGAGC GATATTGCGG 300
   TCATTATCTG CGTGCGCTGC GGCAAGATAG CCTGATAATA AGACTGATCG 350
50 CATAGAGGGG TGGTATTTCA CACCGCCCAT TGTCAACAGG CAGTTCAGCC 400
   TCGTTAAATT CAGCATGGGT ATCACTTATG AAAATTTCATC TACATTGGTG 450
   ATAATAGTAA ATCCAGTAGG GCGAAATAAT TGACTGTAAT TTACGGGGCA 500
   AAACGGCACA ATCTCAAACG AGATTGTGCC GTTTAAGGGG AAGATTCTAG 550
   AAATATTTCA TACTTCCAAC TATATAGTTA AGGAGGAGAC TGAAAATGAA 600
55 GAAGTTGTTT TTTTATTGT TATTGTTATT CTTAATATAC TTAGGTTATG 650
   ACTACGTTAA TGAAGCACTG 670

```

60 2) INFORMATION FOR SEQ ID NO: 1076

610

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: Z36901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

```

ATGAAAATAA TAATTTT TAG AGTGCTAACT TTTTCTTTG TTATCTTTTC      50
TGTTAATGTG GTTGCGAAGG AATTTACCTT AGATTTCCTCG ACAGCAAAGA      100
CGTATGTAGA TTCGCTGAAT GTCATTCGCT CTGCAATAGG TACTCCATTA      150
20 CAGACTATTT CATCAGGAGG TACGTCTTTA CTGATGATTG ATAGTGGCAC      200
AGGGGATAAT TTGTTTGCAG TTGATGTCAG AGGGATAGAT CCAGAGGAAG      250
GGCGGTTTAA TAATCTACGG CTTATTGTTG AACGAAATAA TTTATATGTG      300
ACAGGATTTG TTAACAGGAC AAATAATGTT TTTTATCGCT TTGCTGATTT      350
TTCACATGTT ACCTTTCCTG GTACAACCTGC GGTTACATTG TCTGGTGACA      400
25 GTAGCTATAC CACGTTACAG CGTGTTGCGG GGATCAGTCG TACGGGGATG      450
CAGATAAATC GCCATTTCGT GACTACTTCT TATCTGGATT TAATGTCGCA      500
TAGCGGAACC TCACTGACGC AGTCTGTGGC AAGAGCGATG TTACGGTTTG      550
TTACTGTGAC AGCTGAAGCT TTACGTTTTT GCCAAATTCA GAGGGGATTT      600
CGTACAACAC TTGATGATCT CAGTGGGCGT TCTTATGTAA TGACTGCTGA      650
30 AGATGTTGAT CTTACGTTGA ACTGGGGAAG GTTGAGTAGT GTCCTGCCTG      700
ACTATCATGG ACAAGACTCT GTTCGTGTTG GAAGAATTTC TTTTGGAAGT      750
GTTAATGCAA TTCTGGGTAG CGTGGCATTA ATACTGAATT GTCATCATCA      800
TGCATCGCGA GTTGCCAGAA TTGTACCTAA TGAGTTTCCT TCTATGTGCC      850
CGGTAGATGG AAGAGTGCCT GGGATTACGC ACAATAAAAT ATTGTGGGAC      900
35 TCATCCACTC TGGGGGCAAT TTTGATACGC AGGGCTATTA GCAGTTGA      948

```

2) INFORMATION FOR SEQ ID NO: 1077

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

```

CACCTGTATA TGAAGTGTAT ATTATTTAAA TGGGTACTGT GCCTGTTACT      50
GGGTTTTTCT TCGGTATCCT ATTCCCGGGA GTTTACGATA GACTTTTCGA      100
CCCAACAAAG TTATGTCTCT TCGTTAAATA GTATACGGAC AGAGATATCG      150
ACCCCTCTTG AACATATATC TCAGGGGACC ACATCGGTGT CTGTTATTAA      200
60 CCACACCCCA CCGGGCAGTT ATTTTGCTGT GGATATACGA GGGCTTGATG      250

```



```

TCTATCAGGC GCGTTTTGAC CATCTTCGGC TGATTATTGA GCAAAATAAT 300
TTATATGTGG CCGGGTTCGT TAATACGGCA ACAAATACTT TCTACCGTTT 350
TTCAGATTTT ACACATATAT CAGTGCCCGA TGTGACAACG GTTTCATGA 400
CAACGGACAG CAGTTATACC ACTCTGCAAC GTGTGCGCAGC GCTGGAACGT 450
5 TCCGGAATGC AAATCAGTCG TCACTCACTG GTTTCATCAT ATCTGGCGTT 500
AATGGAGTTC AGTGGTAATA CAATGACCAG AGATGCATCC AGAGCAGTTC 550
TGC GTTTTTGT CACTGTCACA GCAGAAGCCT TACGCTTCAG GCAGATACAG 600
AGAGAATTTT GTCAGGCACT GTCTGAAACT GCTCCTGTGT ATACCATGAC 650
GCCGGGAGAC GTGGACCTCA CTCTGAACTG GGGGCGAATC AGCAATGTGC 700
10 TTCCGGAGTA TCGGGGAGAG GATGGTGTCA GAGTGGGGAG AATATCCTTT 750
AATAATATAT CAGCGATACT GGGTACTGTG GCCGTTATAC TGAATTGCCA 800
TCATCAGGGG GCGCGTTCTG TTCGCGCCGT GAATGAAGAG AGTCAACCAG 850
AATGTCAGAT AACTGGCGAC AGGCCCGTTA TAAAAATAAA CAATACATTA 900
TGGGAAAGTA ATACAGCTGC AGCGTTTCTG AACAGAAAGT CACAGTTTTT 950
15 ATATACAACG GGTAATAAAA GGAGTTAAGT ATGAAGAAGA TGTTTATGGC 1000
GGTTTTATTT GCATTAGTTT CTGTTAATGC AATGGCGGCG GATTGTGCTA 1050
AAGGTAAAAA TGAGTTTTC AAGTATAATG AGGATGACAC ATTTACAGTG 1100
AAGGTTGACG GGAAAGAATA CTGGACCACT CGCTGGAATC TGCAACCGTT 1150
ACTGCAAAGT GCTCAGCTGA CAGGAATGAC TGTCACAATC AAATCCAGTA 1200
20 CCTGTGAATC AGGCTCCGGA TTTGCTGAAG TGCAGTTTAA TAATGACTGA 1250
GGCATAACC 1259

```

25 2) INFORMATION FOR SEQ ID NO: 1078

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40 2) INFORMATION FOR SEQ ID NO: 1079

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55 2) INFORMATION FOR SEQ ID NO: 1080

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 25 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

TATAGCTACT GTCACCAGAC AATGT

25

2) INFORMATION FOR SEQ ID NO: 1081

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA

20

2) INFORMATION FOR SEQ ID NO: 1082

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40

TTGARCRAAA TAATTTATAT GTG

23

2) INFORMATION FOR SEQ ID NO: 1083

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

55

TGATGATGRC AATTCAGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

CTACTCCCGC CTTTGGGTT

20

2) INFORMATION FOR SEQ ID NO: 1087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

CTCACAGCCC GAAACAGCCT

20

5 2) INFORMATION FOR SEQ ID NO: 1088

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20 TCGGCAAGAC AATATGACAG C

21

2) INFORMATION FOR SEQ ID NO: 1093

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSSa-165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40	TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
	AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
	ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
	CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
45	TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	AAAGGAAATG	250
	AATCATGAAA	CAATTAACCTA	AGCCTTTATA	CTTTTACCTA	TTACTTTTTA	300
	TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
	AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAAACAG GTACTTCTAA CTA .

23

2) INFORMATION FOR SEQ ID NO: 1095

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

TCTTCAAAAT CGAAAAAGCC GTC

23

2) INFORMATION FOR SEQ ID NO: 1099

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

TCAAAAGGGA TCACWAAAGT MAC

23

2) INFORMATION FOR SEQ ID NO: 1100

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

GTAAAKCCCG GCATRGTRTT GATTTC

26

2) INFORMATION FOR SEQ ID NO: 1101

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

GACGGYTTTT TYGATTTTGA AGA

23

2) INFORMATION FOR SEQ ID NO: 1102

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

23

15

2) INFORMATION FOR SEQ ID NO: 1103

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

20

30

2) INFORMATION FOR SEQ ID NO: 1104

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

20

45

2) INFORMATION FOR SEQ ID NO: 1105

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

50 CTCCTACGAT TCTCTTGAYA AATCA

25

2) INFORMATION FOR SEQ ID NO: 1106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

CAACCGATCT CAACACCGGC AAT

23

2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

CTCATTTGAC TTCCTCCTTT GCT

23

2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

GTAAGAATCG GAAAAGCGGA AGG

23

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

2) INFORMATION FOR SEQ ID NO: 1110

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

CTTTTCCGG CTCGWYTTCC TGATG

25

2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

GGCTGYGATA TTCAAAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

40 TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

55

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

60 2) INFORMATION FOR SEQ ID NO: 1117

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: 94
 (C) ACCESSION NUMBER: U94526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

15 AAATTCGATC CGCACTACAT CGGAATTACA AAAAACGGTG TATGGAAGCT 50
 ATGCAAGAAG CCATGTACGG AATGGGAAGC CGACAGTCTC CCCGCCATAC 100
 TCTCCCCGGA TAGGAAAACG CATGGGCTGC TTGTCATGAA AGAAAGCGAA 150
 20 TACGAAACAC GCGGTATTGA TGTGGCTTTC CCGGTTTTGC ATGGCAAATG 200
 CGGGGAGGAT GGTGCGATAC AGGGGCTGTT TGTATTGTCT GGTATCCCCT 250
 ATGTGGGCTG TGATATTCAA AGCTCCGCAG CTTGCATGGA CAAATCACTG 300
 GCCTACATTC TTACAAAAAA TCGGGGCATC GCCGTTCCCG AATTTCAAAT 350
 GATTGATAAA GGTGACAAGC CGGAGGCGGG TCGCCTTACC TACCCTGTCT 400
 25 TTGTGAAGCC GGCACGGTCA GGTTTCGTCTT TTGGCGTAAC CAAAGTAAAC 450
 GGTACGGAAG AACTTAACGC TGCGATAGAA GCGGCAGGAC AATATGATGG 500
 AAAAATCTTA ATTGAGCAAG CGATTTCGGG CTGTGAGGTC GGGTGTGCGG 550
 TCATGGGGAA CGAGGATGAT TTGATTGTCT GCGAAGTGGA TCAAATCCGG 600
 CTGAGCCACG GTATCTTCCG CATCCATCAG GAAAACGAGC CGGAAAAAGG 650
 30 CTCAGAAAAT GCGATGATTA CAGTTCCCGC AGACATTCCG GTCGAGGAAC 700
 GAAATCGGGT GCAGGAAACG GCAAAGAAAG TATATCGGGT GCTTGGATGC 750
 AGAGGGCTTG CCCGTGTTGA TCTTTTTTTG CAGGAGGATG GCGGCATCGT 800
 T 801

2) INFORMATION FOR SEQ ID NO: 1118

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

TTTTCWGAGC CTTTTTCCGG CTCG

24

2) INFORMATION FOR SEQ ID NO: 1119

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC

25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG

24

25 2) INFORMATION FOR SEQ ID NO: 1121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

TGTTTGWATT GTCYGGYATC CC

22

40

2) INFORMATION FOR SEQ ID NO: 1122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCATTG CTACGTGG

18

55

2) INFORMATION FOR SEQ ID NO: 1123

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 22 bases

624

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

TTTCGGGCTG TGAGGTCGGB TG

22

10

2) INFORMATION FOR SEQ ID NO: 1124

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTTGRTCC ACYTCGCCRA CA

22

2) INFORMATION FOR SEQ ID NO: 1125

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40

ACTCACAAC TGGGATGGATG

20

45 2) INFORMATION FOR SEQ ID NO: 1126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

TTATGGTTGT GCTGGTTGAG G

21

60

2) INFORMATION FOR SEQ ID NO: 1127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

2) INFORMATION FOR SEQ ID NO: 1128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

2) INFORMATION FOR SEQ ID NO: 1129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

ATGATGACHG AMATGATGAA AAC

23

2) INFORMATION FOR SEQ ID NO: 1130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130

GACTATCCAA GCATGCATTA TG

22

5 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

20

35

2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

50

2) INFORMATION FOR SEQ ID NO: 1134

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAAACCTT CCT

23

2) INFORMATION FOR SEQ ID NO: 1135

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

20 CATTATGCAA ACGCCATTTT AAG

23

25 2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

35 ACTTGTCAC GTTSGATRTC T

21

40 2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

50 AATTAATGGC TGCWGTTGAY GAA

23

55 2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 bases

628

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

	ATGAAAAAAAA	TTGCCGTTTT	ATTTGGAGGG	AATTCTCCAG	AATACTCAGT	50
	GTCAC TAACC	TCAGCAGCAA	GTGTGATCCA	AGCTATTGAC	CCGCTGAAAT	100
15	ATGAAGTAAT	GACCATTGGC	ATCGCACCAA	CAATGGATTG	GTATTGGTAT	150
	CAAGGAAACC	TCGCGAATGT	TCGCAATGAT	ACTTGGCTAG	AAGATCACAA	200
	AAACTGTCAC	CAGCTGACTT	TTTCTAGCCA	AGGATTTATA	TTAGGAGAAA	250
	AACGAATCGT	CCCTGATGTC	CTCTTTCCAG	TCTTGCATGG	GAAGTATGGC	300
	GAGGATGGCT	GTATCCAAGG	ACTGCTTGAA	CTAATGAACC	TGCCTTATGT	350
20	TGGTTGCCAT	GTCGCTGCCT	CCGCATTATG	TATGAACAAA	TGGCTCTTGC	400
	ATCAACTTGC	TGATACCATG	GGAATCGCTA	GTGCTCCCAC	TTTGCTTTTA	450
	TCCCGCTATG	AAAACGATCC	TGCCACAATC	GATCGTTTTA	TTCAAGACCA	500
	TGGATTCCCG	ATCTTTATCA	AGCCGAATGA	AGCCGGTTCT	TCAAAAGGGA	550
	TCACAAAAGT	AACTGACAAA	ACAGCGCTCC	AATCTGCATT	AACGACTGCT	600
25	TTTGCTTACG	GTTCTACTGT	GTTGATCCAA	AAGGCGATAG	CGGGTATTGA	650
	AATTGGCTGC	GGCATCTTAG	GAAATGAGCA	ATTGACGATT	GGTGCTTGTG	700
	ATGCGATTTT	TCTTGTCGAC	GGTTTTTTTG	ATTTTGAAGA	GAAATACCAA	750
	TTAATCAGCG	CCACGATCAC	TGTCCCAGCA	CCATTGCCTC	TCGCGCTTGA	800
	ATCACAGATC	AAGGAGCAGG	CACAGCTGCT	TTATCGAAAC	TTGGGATTGA	850
30	CGGGTCTGGC	TCGAATCGAT	TTTTTCGTCA	CCAATCAAGG	AGCGATTAT	900
	TTAAACGAAA	TCAACACCAT	GCCGGGATTT	ACTGGGCACT	CCCGTACCC	950
	AGCTATGATG	GCGGAAGTCG	GGTTATCCTA	CGAAATATTA	GTAGAGCAAT	1000
	TGATTGCACT	GGCAGAGGAG	GACAAACGAT	GA		1032

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1768 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 50 (C) ACCESSION NUMBER: X56895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

	GATATCGTTA	CGCTTCATGT	GCCGCTCAAT	ACGGATACGC	ACTATATTAT	50
55	CAGCCACGAA	CAAATACAGA	GAATGAAGCA	AGGAGCATTT	CTTATCAATA	100
	CTGGGCGCGG	TCCACTTGTA	GATACCTATG	AGTTGGTTAA	AGCATTAGAA	150
	AACGGGAAAC	TGGGCGGTGC	CGCATTGGAT	GTATTGGAAG	GAGAGGAAGA	200
	GTTTTTCTAC	TCTGATTGCA	CCCAAAAACC	AATTGATAAT	CAATTTTCTAC	250
	TTAAACTTCA	AAGAATGCCT	AACGTGATAA	TCACACCGCA	TACGGCCTAT	300
60	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAACTG	350

	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	400
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	450
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	500
	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	550
5	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	600
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	650
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	700
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	750
	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	800
10	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	850
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	900
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	950
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	1000
	GCTGTTTCGG	GCTGTGAGGT	CGGTGTGCG	GTATTGGGAA	ACAGTGCCGC	1050
15	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	1100
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	1150
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	1200
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCCGTGTGG	1250
	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1300
20	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1350
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1400
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTTAGAT	GAAATAGTAC	1450
	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1500
	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAGTT	1550
25	GGCTGAATCG	CTTTTGAAGG	CAAAAGAACT	GGCTGCTACC	CAAGGGTACG	1600
	GATTGCTTCT	ATGGGACGGT	TACCGTCCTA	AGCGTGCTGT	AAACTGTTTT	1650
	ATGCAATGGG	CTGCACAGCC	GGAAAATAAC	CTGACAAAGG	AAAGTTATTA	1700
	TCCCAATATT	GACCGAACTG	AGATGATTTC	AAAAGGATAC	GTGGCTTCAA	1750
	AATCAAGCCA	TAGCCGCG				1768

2) INFORMATION FOR SEQ ID NO: 1140

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (C) ACCESSION NUMBER: L29638

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

	GTAAGAATCG	GAAAAGCGGA	AGGAAGAAAA	ACATGAAAAA	AATCGCCATT	50
50	ATTTTTTGAG	GCAATTCACC	GGAATACACC	GTTTCTTTAG	CTTCAGCAAC	100
	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	CTATGACTAC	GACCTCTCTT	150
	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	GGTACTTGTA	TACAGGAGAA	200
	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	TTGGATACGA	AACATAAACA	250
	GAAAATACAG	CCGCTATTCT	AAGGAAACGG	CTTTTGGCTA	AGTGAAGAGC	300
55	AGCAAACGTT	GGTACCTGAT	GTTTTATTTC	CCATTATGCA	TGGCAAATAC	350
	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	GAATTGATGA	AGCTGCCTTA	400
	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	ATGTATGAAC	AAATGGCTGC	450
	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	AAAGTGCTCC	TACGATTCTC	500
	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	ATCGAAGCTT	TTATCCAGAC	550
60	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	TGAAGCGGGC	TCCTCAAAG	600

	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	TCGCTTCTGC	CTTAAAAGAA	650
	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	CAAAAAAATA	TTGCCGGTGT	700
	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	CTCTTTGACT	GTCGGTGCTT	750
	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	TCGATTTTGA	AGAAAAGTAC	800
5	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	GCGCCATTGC	CTGAAACGAT	850
	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	GCTCTATCGT	AGTCTTGGTC	900
	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	TCACGGAGCG	AGGAGAACTA	950
	TACTTGAATG	AAATCAATAC	TATGCCGGGC	TTTACGAGTC	ACTCCCGCTA	1000
	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	CTATCAAGAA	CTACTACAAA	1050
10	AACTGCTTGT	CTTAGCAAAG	GAGGAAGTCA	AATGAG		1086

2) INFORMATION FOR SEQ ID NO: 1141

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: extracted from M97297

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

30	ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
	TGCATTCCAT	GCTCTTTCGC	CTCGCTTTGG	CGTTATGGCA	ACGATAATTA	100
	ACGCCAACGT	GTCGGAATCC	AACGCCAAAT	CCGCGCCTTT	CAATCAATGT	150
	ATCAGTGTGG	GACATAAATC	AGAGATTTCC	GCCTCTATTC	TTCTTGCGCT	200
	GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
35	ATATAGATAC	AACTGCTGCT	AAGAGAATGG	GCATCACTGT	CGACAATGTG	300
	GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTCTTAT	350
	GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
	TCAGGTTGGA	CAGCGACCGT	GGCAAGGTAC	TCAGCGACAT	GACAGTTGGT	450
	GTGGTGGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
40	ATTTGGATGT	AAAGTGTTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
	ACTATGTACC	GTTTGATGAG	TTGCTGCAAA	ATAGCGATAT	CGTTACGCTT	600
	CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
	ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
	TTGTAGATAC	CTATGAGTTG	GTTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
45	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
50	TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
	TGCTATTTCAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
55	CTTTGCAATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
60	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550

	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
5	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCG	TGTGGATATG	TTTTTACAAG	1850
	ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
10	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGGAAAACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
	GAAGGCAAAA	GAACCTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	CTGTAAACT	GTTTTATGCA	ATGGGCTGCA	2250
15	CAGCCGGA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAAG	GATACGTGGC	TTCAAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
20	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
	CGGCAGGAAA	CCCGACGTAT	GTAAGTGGT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
25	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GAATGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCAT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACTTATGA	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	2900
	TCCAGTAGGG	CGAAATAATT	GACTGTAATT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTAT	3000
30	ACTTCCAAC	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAATT	ATGATCAAAA	3150
	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
35	AGTAAATATC	CTGTTTCGCCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
40	TACCAGCAGG	TTATAGTGAG	CATAATTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAAATGGA	ACGAGCCCCCT	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTCGCTA	TGTTGGTTTA	3700
	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
45	GGATTACCTA	AAAGAAGAAA	AAACCAATTC	TGTTAGTGTA	AATGGGGAAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTTACTA	AAAATACCAC	CATTCATGTG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAAGG	AGGTAA	3946

50

2) INFORMATION FOR SEQ ID NO: 1142.

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

5

2) INFORMATION FOR SEQ ID NO: 1143

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

CAATTAGCTT AGCAATAGGT GTTGG

25

20

2) INFORMATION FOR SEQ ID NO: 1144

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

TGTYTTCCAA GGTTCAGCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

50

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

60

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40

GACTTTGTTT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

2) INFORMATION FOR SEQ ID NO: 1151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

2) INFORMATION FOR SEQ ID NO: 1152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

2) INFORMATION FOR SEQ ID NO: 1153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

CTCGTATGTC CCTACAATGC

2) INFORMATION FOR SEQ ID NO: 1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

GTTTGAAGCA TATAGCCTCG

20

2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

CAGTGCTTCA TTAACGTAGT C

21

2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

GTTGAAATGC ATCACGAACA ATT

23

2) INFORMATION FOR SEQ ID NO: 1157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

2) INFORMATION FOR SEQ ID NO: 1158

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

TGAAGGTTTG CCAGGTGA

18

2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

CGTTTCTGTT AAAGAAATTA GAAG

24

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

637

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

GTTGGTTTCA ACGTTAAGAA C

21

2) INFORMATION FOR SEQ ID NO: 1164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

GGTTTCAACG TCAAGAAC

18

2) INFORMATION FOR SEQ ID NO: 1165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

2) INFORMATION FOR SEQ ID NO: 1166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

2) INFORMATION FOR SEQ ID NO: 1167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

2) INFORMATION FOR SEQ ID NO: 1168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

GAACAATTGG TTGAAGGTGT

2) INFORMATION FOR SEQ ID NO: 1169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: SP-665
 (C) ACCESSION NUMBER: AF139883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

20	ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
	CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
	ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
	ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
25	TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
	TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
	ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
	TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
	ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
30	GCTTG GTTAG	CGATT CAGTT	AGAACA AAAA	GCAACCAAAC	AGGAAATCTT	500
	GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
	AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
	CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
	CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
35	CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
	GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
	TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
	AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
	AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
40	TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
	TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGAGAG	TCGTCACCAA	1050
	GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
	CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
	ACGGTGTTTA	TGATTCACCT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
45	TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCCG	1250
	TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
	TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
	GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
	TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
50	CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
	TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
	TGTCGGAACT	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
	TGATGAAAAC	AGTCTTGACT	TATGGAAC TG	GGCGTGGAGC	CTATCTTCCT	1650
	TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
55	AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
	TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCG	1800
	AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCTAGTTG	CAGCTAAAGT	1850
	TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
	GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGAATTTGT	ATTCAAAAAT	1950
60	GGAGCTCGCC	CAATATGGAC	TGAACCTCT	ACTCAACAAT	CCTCAACAGC	2000

TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

5

2) INFORMATION FOR SEQ ID NO: 1170

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

40 2) INFORMATION FOR SEQ ID NO: 1172

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: 64147
 (C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

GATCCTCTAA	ATGATTCTCA	GGTGGCTGTT	ATTGCCTCTA	TTTCAAAGGA	50
GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	GGATAGAAAG	GTTTTGGAAA	100
CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	CCAGTGAAAA	AGCTGGTCTC	150
60 CCAGCGGAAG	AAGCAGAAGC	CTATCTTAA	AAAGGCTATT	CTCTAAATGA	200

641

	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
5	TCAATTCAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCTAT	450
	GCAGTCGCCC	TTAACCCTAA	AACAGGTGCT	GTTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTCTAGG	AATCAGACCT	TGACAGACCA	650
10	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCTTGG	TATCCTGCCT	700
	TTTCTAGACC	AATGCCGATT	ACGGCGGTTT	AGGCTCTAGA	GTATTCATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCCTAGGT	CTTATGGGGC	AGACCTATCA	800
	ACCCAATATG	TTTGTCTGGA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
15	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	AAAGAGTATA	GCTTTGCTAA	950
	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAATAATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	ATGGTGTTCG	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	GATAAGGGAG	GACTGGGTGA	1100
	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
20	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
	ACTAGTGAAT	TGACAACTGG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAATGGTGT	1400
25	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

30

2) INFORMATION FOR SEQ ID NO: 1173

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2007 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: CS109
 45 (C) ACCESSION NUMBER: Z49096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
50	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
55	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGTCTA	350
	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAACCTC	400
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGCAATTA	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGAATCTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
60	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600

	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
5	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	850
	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTG GTTG	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
10	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	1100
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
15	AGTTGGGACG	GACCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1350
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1400
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTG GTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
20	GGAGAATTTG	CCACCCCAAT	CTTGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
25	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1850
	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
30	TAATATG					2007

2) INFORMATION FOR SEQ ID NO: 1174

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTCGC

18

2) INFORMATION FOR SEQ ID NO: 1175

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

GTTACTGGTG TAGAAATGTT C

21

5 2) INFORMATION FOR SEQ ID NO: 1176

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20

2) INFORMATION FOR SEQ ID NO: 1177

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

20

35

2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2456 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC8325
(C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

55	ATGAACTGAT	TATACTTAAC	ATTAAAAAAG	ATGATAACAC	CTTCTACACC	50
	TCCATATCAC	AAAAAATTAT	AACATTATTT	TGACATAAAT	ACTACATTTG	100
	TAATATACTA	CAAATGTAGT	CTTATATAAG	GAGGATATTG	ATGAAAAAGA	150
	TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	GTTTGGTATA	200
	TATTTTATG	CTTCAAAAGA	TAAAGAAATT	AATAATACTA	TTGATGCAAT	250
	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	TATATTTCTA	300
60	AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	AAAAATATAT	350

	AATAGTTTAG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	AAATAAAAAA	400
	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	ATTAAAACAA	450
	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	TAAAGAAGAT	500
	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	CAGGAATGCA	550
5	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	CGTGGTAAAA	600
	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	ACATATGAGA	650
	TTAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	AAGCAATCGC	700
	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAACAACAAA	TGGATCAAAA	750
	TTGGGTACAA	GATGATACCT	TCGTTCCACT	TTAAAACCGT	TAAAAAAATG	800
10	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	CAACTAATGA	850
	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	CATCTATTAG	900
	GTTATGTTGG	TCCCATTAAC	TCTGAAGAAT	TAAACAAAAA	AGAATATAAA	950
	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	AAAAACTTTA	1000
	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	ATCGTTGACG	1050
15	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	GAAAAAAGAT	1100
	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	AGAGTATTTA	1150
	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	CACCCCTCAA	1200
	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	CGTCTATCCA	1250
	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	CCGAAGATAA	1300
20	AAAAGAACCT	CTGCTCAACA	AGTTCAGAT	TACAACTTCA	CCAGGTTCAA	1350
	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	AACATTAGAC	1400
	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	AAGATAAATC	1450
	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	GGTAATATCG	1500
	ACTTAAAACA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	TGCTAGAGTA	1550
25	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	AAAAACTAGG	1600
	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	GCTCAAATTT	1650
	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	AGGTTACGGA	1700
	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	TCTATAGCGC	1750
	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACCTTATTA	AAAGACACGA	1800
30	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	TATCAATCTA	1850
	TTAAATGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	AAGAAGATAT	1900
	TTATAGATCT	TATGCAAACCT	TAATTGGCAA	ATCCGGTACT	GCAGAACTCA	1950
	AAATGAAACA	AGGAGAAAGT	GGCAGACAAA	TTGGGTGGTT	TATATCATAT	2000
	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	AAGATGTACA	2050
35	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	AAAGTGTATG	2100
	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	TGAATAACAA	2150
	AACAGTGAAG	CAATCCGTAA	CGATGGTTGC	TTCACTGTTT	TATTATGAAT	2200
	TATTAATAAG	TGCTGTTACT	TCTCCCTTAA	ATACAATTTT	TTCAATTTTCA	2250
	TTGTATGTTG	AAAGTGACAC	TGTAACGAGT	CCATTTTCTT	TTTTTATGGA	2300
40	TTTCTTATTT	GTAATTTCAG	CGATAACGTA	CAATGTATTA	CCTGGTATAC	2350
	AGTTTAATAA	ATTTAACGTT	ATTCATTTGT	GTTCTTGCTA	CAACTTCTTC	2400
	TCCGTATTTA	CCTTCTTCTA	CCCATAATTT	AAATGATATT	GAAAGTGTAT	2450
	GCATGC					2456

45

2) INFORMATION FOR SEQ ID NO: 1179

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

ATTTGGTGAC GGGTGACTTT

60

20

2) INFORMATION FOR SEQ ID NO: 1180

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180
15 TCCACCGTTG CCAATCGCA

19

2) INFORMATION FOR SEQ ID NO: 1181

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181
30 AGCAGCTTAC TAGATGCCGT

20

2) INFORMATION FOR SEQ ID NO: 1182

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182
AACTGCAAGA GATCCTTTGG

20

2) INFORMATION FOR SEQ ID NO: 1183

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2535 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: 175
 (C) ACCESSION NUMBER: M18729

5

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
10	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTTATG	100
	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
15	GTTGTAAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCGA	350
	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGGG	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
20	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
	AGCTTTGAAG	ACCTTCATTT	ATTGGATTTG	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCCTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
25	CTCAGTAAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTTTATG	1000
	ACATTGAGCG	CTTGGCTAGT	CGTGTTTCTT	TTGGCAAAAC	CAATCCAAG	1050
30	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	AGTGTGCCAC	GGATTGCTGC	1100
	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTTGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	CAGAGAAGGG	ACTAGCTGGA	1300
35	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCACGCTC	1350
	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTC	1400
	GCAACTGGGA	AATGTGCCAG	CCCCTTTTTT	CCGCAAGGCG	ACGCTGAAAA	1450
	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	CCCGTATCGA	GGGAGATATG	1500
	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	GAATACGAAA	TATTTATGCG	1550
40	CATTTCGTAA	GAGGTCGGCA	AGTACATCCA	GCGTTTACAA	GCTCTAGCCC	1600
	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	GTCTGGCGGT	TGTGGCTGAA	1650
	ACCCAGCATT	TGATTGACC	TGAGTTTGGT	GACGATTAC	AAATTGATAT	1700
	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAAA	GGTTATGGGG	GCTCAGACCT	1750
	ATATTCCAAA	TACGATTTCAG	ATGGCAGAAG	ATACCAGTAT	TCAATTGGTT	1800
45	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	TATATGCGTC	AGTTAGCCAT	1850
	GACGGCGGTT	ATGGCCCAGC	TGGGTTTCTA	TGTTTCTGCT	GAAAGCGCCC	1900
	ATTTACCGAT	TTTTGATGCG	ATTTTTTACCC	GTATCGGAGC	AGCAGATGAC	1950
	TTGGTTTTCGG	GTCAGTCAAC	CTTTATGGTG	GAGATGATGG	AGGCCAATAA	2000
	TGCCATTTCG	CATGCGACCA	AGAACTCTCT	CATTCTCTTT	GATGAATTGG	2050
50	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	CTCTTGCTCA	GTCCATCATC	2100
	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	ACCCTCTTTG	CGACCCACTA	2150
	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	ACAACACTTG	GTCAATGTCC	2200
	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	TCACCTTCCT	TCACAAGATT	2250
	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	ATCCATGTTG	CCAAGATTGC	2300
55	TGGCTTGCCA	CGAGACCTTT	TAGCAAGGGC	GGATAAGATT	TTGACTCAGC	2350
	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	CCATGAGACA	AACTAGTGCT	2400
	GTCACTGAAC	AGATTTCACT	CTTTGATAGG	GCAGAAGAGC	ATCCTATCCT	2450
	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	TATGACACCT	ATGCAGGTTA	2500
60	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	TATAA		2535

2) INFORMATION FOR SEQ ID NO: 1184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TTG			623

2) INFORMATION FOR SEQ ID NO: 1185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

50	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
55	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
60	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550

CAAGGGTGGT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC T 621

5

2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTCATCG	250
GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGCTACGAAA	300
TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTG	450
ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
CAAGGGTGGT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
AAACCAATCC	AAAGGATCTC	TT			622

35

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCGGT	ATGTTCATCG	250
GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGCTACGAAA	300
TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350

60

	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
5	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
	AAACCAATCC	AAAGGATCTC	TT			622

10 2) INFORMATION FOR SEQ ID NO: 1188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

25	GGGTGACTTT	TATGTAACGG	GGCTATTGGA	TTTCACGTTG	GTTTGTGGGG	50
	AAATTCGCAA	TCTCAAGGCT	AGAGAAGTGG	TGCTGGGTTA	TGACTTGTCT	100
	GAGGAAGAAG	AACAAATCCT	CAGTCGTCAG	ATGAATCTGG	TGCTTCTTTA	150
	TGAGAAGGAA	GGCTTTGAGG	ACCTTCATTT	ACTGGATCCA	CGACTGGCAG	200
30	CTGTGGAGCA	AGCGGCAGCT	AGTAAGCTCC	TCCAGTATGT	TCACCGGACC	250
	CAGATGCGGG	AATTGAACCA	CCTCAAACCA	GTTATCCGCT	ATGAAATCAA	300
	AGATTTCTTA	CAGATGGACT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	350
	AGAATGCCCC	TTCAGGCAAG	AAGCAAGGCA	GTCTTTTCTG	GCTTTTAGAT	400
	GAAACCAAGA	CGGCTATGGG	AATGCGTCTC	TTGCGTTCTT	GGATTCATCG	450
35	TCCTTTGATT	GATAAGGAGC	GAATCGTCCA	GCGTCAAGAG	GTGGTGCAGG	500
	TCTTTCTTGA	CCACTTCTTT	GAGCGTAGTG	ATTTAACGGA	CAGTCTTAAG	550
	GGTGTTTATG	ATATCGAACG	CTTGGCTAGT	CGGGTTTCTT	TTGGCAAGA	599

40 2) INFORMATION FOR SEQ ID NO: 1189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

	GGTGACGGGT	GACTTTTATG	TGACAGGTCT	TTTGATTTTT	ACGCTGGTTT	50
	GTGGGGAAAT	CCGCAATCTC	AAGGCTCGAG	AAGTGGTGCT	GGGTTATGAC	100
	TTGTCTGAGG	AAGAAGAACA	GATCCTTAGT	CGTCAGATGA	ATCTGGTACT	150
60	TTCCTATGAA	AAAGAAGGCT	TTGAAGACCT	TCATTTACTG	GATTCACGAT	200

	TGGCAGCTGT	GGAGCAAGCG	GCATCTAGTA	AACTGCTTCA	GTATGTTTCAT	250
	CGGACTCAGA	TGAGGGAATT	GAACCACCTC	AAGCCTGTTA	TCCGCTATGA	300
	AATCAAAGAT	TTTTTGCAGA	TGGATTATGC	GACCAAGGCT	AGTCTGGATT	350
	TGGTTGAGAA	TGCCCCGTTCA	GGCAAGAAGC	AAGGTAGTCT	TTTTTGGCTT	400
5	TTGGATGAAA	CCAAAACAGC	TATGGGAATG	CGTCTCTTGC	GGTCTTGGAT	450
	TCATCGCCCC	CTGATTGATA	AGGAACGAAT	TGTCCAACGC	CAAGAAGTTG	500
	TGCAGGTCTT	TCTCGACCAT	TTCTTTGAGC	GTAGTGATTT	GACAGACAGT	550
	CTCAAGGGTG	TTTATGACAT	TGAGCGCTTG	GCTAGTCGTG	TTTCTTTTGG	600
	CAAAACCAAT	CCAAAGGATC	TCTT			624

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2) INFORMATION FOR SEQ ID NO: 1190

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGT	CTTGGTCTGC	50
30	GGGGAAATCC	GCAATTGAA	AGCTAGGGAA	GTGGTGCTGG	GCTATGCCTT	100
	GCCAGAAGCT	GAGGAGCAGG	TTTTGGCTGG	ACAGATGAAC	CTTTTACTGT	150
	CCTATGTGGA	GAAGGTTTTC	GAGGATGTTT	AGCTGCTGGG	CGAGGAGCTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCAGGGAAA	CTGCTGGAGT	ATGTGCACCG	250
	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCTCAG	CATTATGAAA	300
35	TCAAGGACTT	CCTGCAAATG	GACTATGCCA	CCAAGGCGAG	TCTGGATTTG	350
	ACAGAAAATG	CTCGCTCGGG	CAAGAAGCAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACT	AAGACGGCCA	TGGGCGGCCG	CATGCTGCGC	TCTTGGATCC	450
	AGCGTCCGCT	GATTGATGAA	GCGCGAATTA	GCCAGCGACA	GAATGTCGTT	500
	GAGGTTTTTC	TGGATCATTT	CTTTGAGCGG	AGTGATTTGA	CGGAGAGCCT	550
40	CAAGGGGGTG	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGC	599

2) INFORMATION FOR SEQ ID NO: 1191

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

60	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGC	CCTGGTCTGC	50
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GGGGAAATCC GTAATTGAA GGCTAGGGAA GTGGTGCTGG GCTATGCTTT 100
GCCAGAAGCT GAGGAGCAGG TCTTGGCTGG ACAGATGAAT CTTTGTCTGT 150
CCTATGTACA GACGGCCTTG GACGATGTCC AGCTGCTGGG CGAGGAACTG 200
TCTCCTATGG AGCGTCAGGC AGCGGGGAAA TTGCTAGAGT ATGTGCACCG 250
5 GACCCAGATG AGGGAGCTCA GCCATTTGAA GAAGGCCAG CATTATGAAA 300
TCAAGGACTT TCTGCAAATG GATTATGCTA CCAAGGCGAG TCTGGATTTG 350
ACAGAAAATG CTCGCTCGGG TAAGAAACAC GGCAGTCTTT ATTGGCTGAT 400
GGACGAGACC AAGACGGCCA TGGGCGGCCG TATGCTGCGC TCTTGGATCC 450
AGCGTCCGTT GATTGATGAA GTGCGAATTA GCCAGCGGCA GAATGTCGTC 500
10 GAGGTTTTTC TGGAACATTT CTTTGAGCGG AGTGATTTGA CGGAGAGCCT 550
CAAGGGAGTC TATGATATCG AGCGGCTGGC TAGTCGGGTG TCTTTTGGCA 600
AGACCAATCC AAAGGATCTC TT 622

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15

2) INFORMATION FOR SEQ ID NO: 1192

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear
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(ii) MOLECULE TYPE: DNA
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

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GGTAAAACAG GAACCTCTAA CT

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22

30

2) INFORMATION FOR SEQ ID NO: 1193

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear
35

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(ii) MOLECULE TYPE: DNA
40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

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GGTAAGACAG GTACTTCTAA CT

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22

45

2) INFORMATION FOR SEQ ID NO: 1194

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear
50

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55

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(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

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60

CATTTC AAGT AATACAACAG AATC

24

5 2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTTC AAGT AACACA ACTG AATC

24

20 2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTC AA GTAATACAAC AGAA

24

35 2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1198

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

	AACGGGCGTC	TCGATAGAAA	AACACGTGAA	AATCCCAATG	ATTATAAACA	50
10	ATCAATATAC	GATTTTGCTG	AAGCTGTAAC	AAAAGGTATT	AAGGAACAAA	100
	CAAATAAAAA	TTAATAGGCA	ACTTAACCAG	AATCGTTAAA	ACTATATGAC	150
	GATTCTGGTT	TTTTAAATTC	AAAAAGTTTT	CTAAAAAATT	TACTTGCTTC	200
	TTTAAAGTAT	AGGTATGAAA	TACAATTGAT	TAAAATAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAATACT	GCCTTTATAC	TTTTACCTAT	TACTTTTTAT	300
15	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTGCCA	ATCACAKGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT	A		381

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC

25

35

2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAAA GCTGT

25

50

2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

GTGTTGAAAT GTTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

GGIGARMGIG GIAAYGARAT G

21

2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

10

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

25

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

40

CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

55

TCAAAAAGTT TTCTAAAAAA TTTAC

25

60 2) INFORMATION FOR SEQ ID NO: 1209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA

2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

2) INFORMATION FOR SEQ ID NO: 1212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

CCICCCIRGIG GIGAIACIGC WCC

2) INFORMATION FOR SEQ ID NO: 1213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

AARGGIGGIA CIGCIGCIAT HCCIGG

26

2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

GGTAAAACAG GTACCTCTAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: D471
- (C) ACCESSION NUMBER: X65717

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

AACAAAATAA	AAGAACTTAC	CTATTTTCCA	TCCAAAATGT	TTAGCAATCA	50
TCATCTGCAA	GGCAACGTAT	TGCATGGCAT	TGATGTGATG	AGCAACTAAT	100
ATGTCATTAG	AACGTTGCGT	CAAAC TAGCA	TCTAAATAAA	GATCGAAATG	150
CAGTTATCAA	AAATGCAAGC	TCCTATCGGC	CCTTGTTTTA	ATTATTACTC	200
ACATTGCCTT	AATGTATTTA	CTTGCTTATT	ATTAAC TTTT	TTGCTAAGTT	250
AGTAGCGTCA	GTTATTCATT	GAAAGGACAT	TATTATGAAA	ATTCTTGTA	300
CAGGCTTTGA	TCCCTTTGGC	GGCGAAGCTA	TTAATCCTGC	CCTTGAAGCT	350
ATCAAGAAAT	TGCCAGCAAC	CATTCATGGA	GCAGAAATCA	AATGTATTGA	400

	AGTTCCAACG	GTTTTTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
	AAAGCTTTCA	ACCTGATGCA	GTCCTTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
	ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
	TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
5	GTAAAGCAGC	TTATTTTTTCA	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
	ATTCATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAATACAG	CTGGTACCTT	700
	TGTTTGCAAT	CATTTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
	GTCCAAATGC	CAAAGCTGGG	TTTATGCATA	TTCCCTTTAT	GATGGAACAG	800
	GTTGTTGATA	AACCTAATAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
10	AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTTCAAA	GATCGTTCCG	900
	ATTTAAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
	TATTTTAAAA	AAACAGAGAT	ATGAACTAAC	TCTGTTTTTT	TTGTGCTAAA	1000
	AATGAAAGAC	CTAGGGAAAC	TTTTCATCGG	TCTTTCTCAA	TTGTCATCTT	1050
	AATCTAATAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
15	AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAAACAT	TAAGGTCAGG	1150
	GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TAACAAAGGA	CTAATATCAT	1200
	AGGTGGCTAC	CACCTTTCCA	GAATCAGGTT	GGAGTTTGAC	AATAGTATTG	1250
	GTTTGCCAAA	TATTGGCATA	GAGATAACCA	TCTACATACT	CTAATTCGTT	1300
20	AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

2) INFORMATION FOR SEQ ID NO: 1216

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1217

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50 CAAATGCCAT TTCAAGTAAC ACAAC

25

55 2) INFORMATION FOR SEQ ID NO: 1218

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

10

2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

GAYACICCI G GICAYGTIGA YTT

23

55

2) INFORMATION FOR SEQ ID NO: 1222

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222

ATYGAYACIC CIGGICAYGT IGAYTT

2) INFORMATION FOR SEQ ID NO: 1223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223

AYITCIARRT GIARYTCRCC CATICC

2) INFORMATION FOR SEQ ID NO: 1224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224

CCIGYIHTIY TIGARCCCIAT IATG

2) INFORMATION FOR SEQ ID NO: 1225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225

TAICCRAACA TYTCISMIAR IGGIAC

2) INFORMATION FOR SEQ ID NO: 1226

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226
15 GTIRMRTAIC CRAACATYTC 20

2) INFORMATION FOR SEQ ID NO: 1227

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227
30 GTICCIYTIK CIGARATGTT YGGITA 26

2) INFORMATION FOR SEQ ID NO: 1228

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228
GTICCIYTIK CIGARATGTT YGGITAYGC 29

2) INFORMATION FOR SEQ ID NO: 1229

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCI GT IATCAT

26

5 2) INFORMATION FOR SEQ ID NO: 1230

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC 150
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA 350
 TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTCAG CCGCAGTCTG 400
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCGCG CATTGCGTTC 450
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTAAACCA 500
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550
 GTGCTGAAGA ACATTTCAAC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700
 35 AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750
 GAAGAACTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850
 GTGTTCAAGC GATGCTGGAT GCGGTAATTG ATTACCTGCC ATCCCCGGTT 900
 GACGTACCTG CGATCAACGG TATCCTGGAC GACGGTAAAG ACACTCCGGC 950
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000
 TCGTACCGA CCCGTTTGTG GGTAACCTGA CTTTCTTCCG TGTTTACTCC 1050
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100
 TGAGCGTTTC GGTCTGATCG TTCAGATGCA CGTAACAAA CGTGAAGAGA 1150
 TCAAAGAAGT TCGCGCGGCG GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200
 45 GTAACCACTG GTGACACCCG GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450
 50 AGCGTGAATT CAACGTTGAA GCGAACGTAG GTAAACCGCA GGTTGCTTAC 1500
 CGTGAAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550
 ACAGTCTGGT GGTCTGTGTC AGTATGGTCA TGTTGTTATC GACATGTACC 1600
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTTG ATAAAGGTAT 1700
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750
 TGGGTATTCT TCTGCACTTC GGTTCCTTACC ATGACGTTGA CTCCTCTGAA 1800
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTAAAGAAG GCTTTAAGAA 1850
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG AACTGAGCCG TCGTCTGGT 1950
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GGCCTTAAGA TCCACGCTGA 2000

AGTACCGCTG	TCTGAAATGT	TCGGATACGC	AACTCAGCTG	CGTTCTCTGA	2050
CCAAAGGTCG	TGCATCATA	ACTATGGAAT	TCCTGAAGTA	TGATGAAGCG	2100
CCGAGTAACG	TTGCTCAGGC	CGTAATTGAA	GCCCGTGGTA	AATAA	2145

5

2) INFORMATION FOR SEQ ID NO: 1231

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

2) INFORMATION FOR SEQ ID NO: 1232

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

2) INFORMATION FOR SEQ ID NO: 1233

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

55 2) INFORMATION FOR SEQ ID NO: 1234

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

664

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

10

2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

25

2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 34 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTCG CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

55

2) INFORMATION FOR SEQ ID NO: 1238

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC

38

2) INFORMATION FOR SEQ ID NO: 1239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC

33

2) INFORMATION FOR SEQ ID NO: 1240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC

38

2) INFORMATION FOR SEQ ID NO: 1241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC

35

2) INFORMATION FOR SEQ ID NO: 1242

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (E) STRAIN: BM4147-1
 (F) ACCESSION NUMBER: U39790

15

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

20	TTCTTAGAGA CATTGAATAT GCCTTATGTC GCGCAGGCG TATTGACCAG	50
	TGCATGTGCC ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG	100
	GTGTGCCGCA AGTTCCTTAT GTACCAGTAC TTAAGAATCA ATGGAAAGAA	150
	AATCCTAAAA AAGTATTTGA TCAATGTGAA GGTTCCTTGC TTTATCCGAT	200
	GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT ACAAAGGCAG	250
25	AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT	300
	TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC	350
	TGTATTAGGA AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA	400
	AAGACGTAGC ATTCTATGAT TATGAAGCCA AATATATCAA TAATAAAATC	450
	GAAATGCAGA TTCCAGCCGA AGTGCCGGA GAAGTTTATC AAAAAGCGCA	500
30	AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC GGATTGAGCC	550
	GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA	600

35 2) INFORMATION FOR SEQ ID NO: 1243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

45

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

50

50	GGTACCAAAG AAAAAAACGA ACGCCACAAC CAACAGCCTC TAAAGCAACA	50
	CCTGCTTCTG AAATTGAGGG AGATTTAGCA AATGTCAATG AGATTCTTTT	100
	GGTTCACGAT GATCGTGTCG GGTCAGCAAC GATGGGAATG AAAGTCTTAG	150
	AAGAAATTTT AGATAAAGAG AAAATTTCAA TGCCGATTCTG AAAAATTAAT	200
55	ATTAATGAAT TAACTCAACA AACACAGGCT TTAATTGTCA CAAAAGCTGA	250
	ACTAACGGAA CAAGCACGTA AAAAAGCACC GAAAGCGACA CACTTATCAG	300
	TAAAAAGTTA TGGTTAATCC CCAAAAATAT GAAACAGTGG GTTTCGCTCT	350
	TAAAAGAAAG TGCCTAGAGA GGAAGAAAAC AATGGAAAAT CTTACGAATA	400
	TTTCAATTGA ATTAAATCAA CAGTTTAATA CAAAAGAAGA AGCTATTCGC	450
60	TTTTCCGGCC AGAAACTAGT CGAGGCAGGC TGTGTTGAGC CCGCTTATAT	500

	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTGAAAAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
	AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
5	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
10	TTAAAAGAAC	GTAAAAGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
	ACAAATTAAC	GTTGAAAATG	TGACCGGGTT	AAATAACATG	ACAGAACCAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCGCTGGAT	ATTATCGCTT	1200
15	GTGAAAATAT	GATTGGTGGT	TCAACCTTTT	TAGCAGAAGA	AGTGGCCATA	1250
	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCCTGATGC	1300
	GGCAGTTGAT	CGGATTGTTC	CATTACAAAA	ACATAAAGAT	CCACTTTTTG	1350
	TTCAAGTTGA	GCCTTTTTGT	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAGTTAGA	AGGCGTCATT	ACTTGTCGAT	TAGAGCCGTA	1450
20	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAATCAGTT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAAATAAAT	ATATTTTCAGA	TGCTATTACA	1700
25	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCGCAAG	AACGGTTTAT	1750
	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCG	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAGATCCAG	AAACGGTTAA	AAATATTAAA	1950
30	CAAAACGTAG	AACTGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACTTTTGG	2100
	AGGTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTAAA	CTTAAACTTG	2150
	TTCATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
35	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
	GAACCTGGTG	AAGAAGGGGG	GATCC			2275

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

55	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATTA	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
60	CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250

ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

2) INFORMATION FOR SEQ ID NO: 1245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAACAGAG	50
CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCCAC	AGATGGACTT	150
20 GTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
ACTTAGATGG	TGAGGTTCCCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
CAAGCACCTG	CATTCGAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
25 TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
30 GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGCCGT	750
ATGCCATCTG	CGGTAGGTTA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800
ATTACAAGAG	CGTATTACAT	CTACAAATAA	AGGGTCTATC	ACGTC	845

2) INFORMATION FOR SEQ ID NO: 1246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 11986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

TGCACTTCAT	TTAGGTGATG	ACACAGTTCG	TACAGTTGCA	ATGTCTTCCA	50
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	CAGATGGACT	TGTTCGTGGC	ACAGAAGTAG	AAGATACTGG	TAAAGCAATC	100
	TCTGTACCAG	TTGGTGATGT	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	150
	TGATGCAATT	GACTTAGATG	GTGATGTTCC	TGCGGATGTA	CGTCGTGATC	200
	CAATTCACCG	TCAAGCGCCT	GCATTCGAAG	AGTTATCTAC	TAAAGTAGAA	250
5	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	300
	GGGTGGTAAG	ATTGGTCTAT	TCGGTGGTGC	CGGCGTAGGT	AAAACAGTAT	350
	TAATTCAGGA	ATTAATTAAT	AACATCGCAC	AAGAGCACGG	TGGTATCTCT	400
	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAAGGTAACG	ACTTATACCA	450
	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	500
10	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCATT	AACAGGTTTA	550
	ACAATGGCTG	AACATTTCCG	TGATGAGCAA	GGACAAGACG	TACTATTGTT	600
	CATCGATAAC	ATCTTCCGTT	TCACGCAAGC	GGGTTCTGAA	GTATCTGCCC	650
	TTCTTG					656

15

2) INFORMATION FOR SEQ ID NO: 1247

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 791 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
25	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Bacillus thuringiensis</i>
	(B) STRAIN: ATCC 10792

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

	CGAAAACGGA	AGTATTAAC	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50	
	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTTCGT	100	
35	GGCACAGAAG	TAGAAGATAC	TGGTAAACCA	ATCTCTGTAC	CAGTTGGTGA	150	
	TGTAACACTT	GGTCGCGTAT	TTAACGTATT	AGGTGATGCA	ATTGACTTAG	200	
	ATGGTGAGGT	TCCTGCAGAT	GTACATCGTG	ATCCAATTCA	CCGTCAAGCA	250	
	CCTGCATTCG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AAACTGGTAT	300	
	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350	
40	TATTCGGTGG	TGCCGGCGTA	GGTAAAACAG	TATTAATTCA	GGAATTAATT	400	
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTCTG	CTGGTGTAGG	450	
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500	
	GCGTAATCAA	GAAAAC	TGCG	ATGGTATTCTG	GACAAATGAA	CGAGCCACCT	550
	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATT	600	
45	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650	
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700	
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750	
	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT	A	791	

50

2) INFORMATION FOR SEQ ID NO: 1248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: BGSC 4AC1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

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15  ATCTACAATG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGCATGAA      50
    CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
    TTGCGATGTC TTCCACAGAT GGACTTGTTT GTGGCACAGA AGTAGAAGAT      150
    ACTGGTAAAG CAATCTCTGT ACCAGTTGGT GATGCAACAC TTGGACGTGT      200
    ATTCAACGTA TTAGGTGATG CAATTGACTT AGATGGTGAA CTTCTGCGG      250
20  ATGTACACCG TGATCCAATT CACCGTCAAG CACCTGCATT CGAAGAATTA      300
    TCTACTAAAG TAGAAATTCT TGAAACTGGT ATTAAAGTAG TAGACTTACT      350
    TGCTCCTTAC ATTAAGGGTG GTAAGATCGG CCTATTCGGT GGTGCCGGCG      400
    TAGGTAAAC AGTATTAATT CAGGAGTTAA TCAATAACAT CGCACAAAGAG      450
    CACGGTGGTA TCTCTGTATT CGCTGGTGTA GGTGAGCGTA CTCGTGAGGG      500
25  TAATGACTTA TACCACGAAA TGAGCGATTC TGGCGTAATC AAGAAAACCTG      550
    CGATGGTATT CGGACAAATG AACGAGCCAC CTGGAGCACG TCAACGTGTT      600
    GCATTAACAG GTTTAACAAT GGCTGAGCAT TTCCGTGATG AGCAAGGACA      650
    AGACGTACTT CTGTTTCATCG ATAACATCTT CCGTTTCACG CAAGCGGGTT      700
    CTGAAGTATC TGCCCTTCTT GGTTCGTATGC CATCTGCGGT AGGTTACCAA      750
30  CCAACACTTG CAACAGAAAT GGGTCAATTA CAAGAGCGTA TTACATCTAC      800
    AAATAAAGGG TCTATCACGT CTATC      825
  
```

35 2) INFORMATION FOR SEQ ID NO: 1249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

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50  ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGTATTAA      50
    CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
    TTGCGATGTC TTCCACAGAT GGACTTGTTT GTGGCACAGA AGTAGAAGAT      150
  
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	ACTGGTAAAC	CAATCTCTGT	ACCAGTTGGT	GATGTAACAC	TTGGTCGCGT	200
	ATTTAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAG	GTTCCTGCAG	250
	ATGTACATCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
5	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAAC	AGTATTAATT	CAGGAATTAA	TTAACAACAT	CGCACAAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
	TAATGACTTA	TACCACGAAA	TGAGCGATTC	TGGCGTAATC	AAGAAAACCTG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
10	GCATTAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTCATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
	CCAACACTTG	CAACAGAAAT	GGGTC			775

15

2) INFORMATION FOR SEQ ID NO: 1250

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10204

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

	CCAGCAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAGC	50
	GAGCATCAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	GATGACACAG	100
35	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTCTG	TGGCACAGAA	150
	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	ATGTAACACT	200
	TGGTCGCGTA	TTCAACGTAT	TAGGTGATGC	AATTGACTTA	GATGGTGATG	250
	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	ACCTGCATTC	300
	GAAGAACTAT	CTACAAGAAT	AGAAATTCTT	GAAACTGGTA	TTAAAGTAGT	350
40	AGATTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACG	GTATTAATTC	AGGAATTAAT	TAACAACATC	450
	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	GTGAGCGTAC	500
	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	GGCGTAATTA	550
	AGAAAACCTGC	GATGGTATTT	GGACAAATGA	ACGAGCCACC	TGGAGCACGT	600
45	CAACGTGTTG	CATTAAACAGG	TTTAACAATG	GCTGAACATT	TCCGTGATGA	650
	GCAAGGACAA	GACGTACTAT	TGTTTCATCGA	TAACATCTTC	CGTTTCACGC	700
	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GTCGTATGCC	ATCTGCGGTA	750
	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	AAGAGCGTAT	800
50	TACATCTACA	AATAAAGGGT	CTATCACGTC	TA		832

2) INFORMATION FOR SEQ ID NO: 1251

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

15 AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100
 AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG 150
 ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC 200
 20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCTGC 250
 AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT 300
 TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA 350
 CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTCT GTGGTGCCGG 400
 CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATTAACAAC ATCGCACAAAG 450
 25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG 500
 GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC 550
 TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG 600
 TTGCATTAAC AGGTTTAACA ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA 650
 CAAGACGTAC TTCTGTTCAT CGATAACATC TTCCGTTTCA CGCAAGCGGG 700
 30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTTACC 750
 AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT 800
 AC 802

35

2) INFORMATION FOR SEQ ID NO: 1252

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1410

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100

	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	GAAGTAGAAG	150
	ATACTGGTAA	ACCAATCTCT	GTACCAGTTG	GTGATGTAAC	ACTTGGTCGC	200
	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	AGGTTCTCTGC	250
	AGATGTACAT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	TTCGAAGAAT	300
5	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	AGTAGACTTA	350
	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTTCG	GTGGTGCCGG	400
	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATTAACAAC	ATCGCACAAAG	450
	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	TCAAGAAAAC	550
10	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	CGTCAACGTG	600
	TTGCATTAAC	AGGCTTAACA	ATGGCTGAGC	ATTTCCGTGA	TGAGCAAGGA	650
	CAAGACGTAC	TTCTGTTTCA	CGATAACATC	TTCCGTTTCA	CGCAAGCGGG	700
	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	GTAGGTTACC	750
	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	TATTACATCT	800
15	ACAAATAAAG	GGTCTATCAC	GTC			823

2) INFORMATION FOR SEQ ID NO: 1253

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

35	CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	CATGAACCTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCTGGG	CACAGAAGTA	150
	GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTTGGTGATG	CAACACTTGG	200
	ACGTGTATTC	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAACCTC	250
40	CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCCTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
	CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AATTAATCAA	TAACATCGCA	450
	CAAGAGCATG	GTGGTATCTC	TGTATTTCGT	GGTGTAGGTG	AGCGTACTCG	500
45	TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTCGAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
50	TACCAACCGA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATT	798

2) INFORMATION FOR SEQ ID NO: 1254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	ACACAGTTCG	TACAGTTGCA	50
ATGTCTTCCA	CAGATGGACT	TGTTTCGTGGC	ACAGAAGTAG	AAGATACTGG	100
TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	AACACTTGGT	CGTGTATTTA	150
ACGTATTAGG	TGATGCAATT	GACTTAGATG	GTGAGGTTCC	TGCGGATGTA	200
CGTCGTGATC	CAATTCACCG	TCAAGCACCT	GCATTCGAAG	AATTATCTAC	250
TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	300
CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	TCGGTGGTGC	CGGTGTAGGT	350
AAAACGGTAT	TAATTCAGGA	ATTAATCAAT	AACATCGCAC	AAGAACACGG	400
TGGTATCTCT	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAGGGTAATG	450
ACTTATACCA	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	500
GTATTCGGAC	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCGTT	550
AACAGGTTTA	ACAATGGCTG	AGCATTTCCG	TGATGAGCAA	GGACAAGACG	600
TACTTCTGTT	CATCGATAAT	ATCTTCCGTT	TCACGCAAGC	AGGTTCTGAA	650
GTATCTGCCC	TTCTTGGCCG	TATGCCATCT	GCGGTAGGTT	ACCAACCAAC	700
ACTTGCAACA	GAAATGGGTC	AATTACAAGA	GCGTATTACA	TCTACAAATA	750
AAGGGTCTAT	CACGTCT				767

2) INFORMATION FOR SEQ ID NO: 1255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: C-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

GAAATGCGTG	AATCATTTTT	AGATTATGCG	ATGAGTGTTA	TCGTTGCTCG	50
TGCATTGCCA	GATGTTTCGTG	ACGGTTTAAA	ACCAGTACAT	CGTCGTATAC	100

	TATATGGATT	AAATGAACAA	GGTATGACAC	CGGATAAATC	ATATAAAAAA	150
	TCAGCACGTA	TCGTTGGTGA	CGTAATGGGT	AAATATCACC	CTCATGGTGA	200
	CTTATCTATT	TATGAAGCAA	TGGTACGTAT	GGCTCAAGAT	TTCAGTTATC	250
	GTTATCCGCT	TGTTGATGGC	CAAGGTAAC	TTGGTTCAAT	GGATGGAGAT	300
5	GGCGCAGCAG	CAATGCGTTA	TACTGAAGCG	CGTATGACTA	AAATCACACT	350
	TGAACTGTTA	CGTGATATTA	ATAAAGATAC	AATAGATTTT	ATCGATAACT	400
	ATGATGGTAA	TGAAAGAGAG	CCGTCAGTCT	TACCTGCTCG	ATTCCCTAAC	450
	TTATTAGCCA	ATGGTGCATC	AGGTATCGCG	GTAGGTATGG	CAACGAATAT	500
	TCCACCACAT	AACTTAACAG	AATTAATCAA	TGGTGTACTT	AGCTTAAGTA	550
10	AGAACCCTGA	TATTTCAATT	GCTGAGTTAA	TGGAGGATAT	TGAAGGTCCT	600
	GATTTCCCAA	CTGCTGGACT	TATTTTAGGT	AAGAGTGGTA	TTAGACGTGC	650
	ATATGAAACA	GGTCGTGGTT	CAATTCAAAT	GCGTTCTCGT	GCAGTTATTG	700
	AAGAACGTGG	AGNCGGACGT	CAACGTATTG	TTGTCACTGA	AATTCCTTTC	750
	CAAGTGAATA	AGGCTCGTAT	GATTGAAAAA	ATTGCAGAGC	TCGTTCTGTA	800
15	CAAGAAAATT	GACGGTATCA	CTGATTTACG	TGATGAAACA	AGTTTACGTA	850
	CTGGTGTGCG	TGTCGTTATT	GATGTGCGTA	AGGATGCAAA	TGCTAGTGTC	900
	ATTTTAAATA	ACTTATACAA	ACAAACACCT	CTTCAAACAT	CATTTGGTGT	950
	GAATATGATT	GCACTTGTA	ATGGTAGACC	GAAGCTTATT	AATTTAAAAG	1000
	AAGCGTTGGT	ACATTATTTA	GAGCATCAAA	AGACAGTTGT	TAGAAGACGT	1050
20	ACGCAATACA	ACTTACGTAA	AGCTAAAGAT	CGTGCCCA	TTTGTAGAAGG	1100
	ATTACGTATC	GCACTTGACC	ATATCGATGA	AATTATTTC	ACGATTCGTG	1150
	AGTCAGATAC	AGATAAAGTT	GCAA			1174

25

2) INFORMATION FOR SEQ ID NO: 1256

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10209

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAGCAAGCAT	50
	TAACTTAACA	TTTGAAGTTG	CACTTCATTT	AGGTGATGAC	ACAGTTCGTA	100
	CAGTTGCAAT	GTCTTCCACA	GATGGACTTG	TTCGTGGCAC	AGAAGTAGAA	150
45	GATACTGGTA	AAGCAATCTC	TGTACCAGTT	GGTGATGTAA	CACTTGGTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGA	GATGTTCTTG	250
	CGGATGTACG	TCGTGATCCA	ATTCACCGTC	AAGCGCCTGC	ATTCGAAGAG	300
	TTATCTACTA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
	ACTTGCTCCT	TACATTAAGG	GTGGTAAGAT	CGGTCTATTC	GGTGGTGCCG	400
50	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTAATCGTGA	500
	AGGTAACGAC	TTATACCACG	AAATGAGCGA	TTCTGGCGTA	ATTAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGAGC	ACGTCAACGT	600

GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
GCAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
GTTCTGAAGT	ATCTGCCCTT	CTTGGTCGTA	TGCCATCTGC	GGTAGGTTAC	750
CAGCCAACAC	TTGCAACAGA	AATGGGTCAA			780

5

2) INFORMATION FOR SEQ ID NO: 1257

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 7700

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	ACGAAAACGG	50
25 AACAAGCATT	AACCTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGACA	100
CAGTTCGTAC	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
ACTTGGTCGT	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
AGGTTCTTGC	GGATGTACGT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
30 TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGTCTATTTCG	400
GTGGTGCCGG	TGTAGGTAAA	ACGGTATTAA	TTCAGGAATT	AATCAATAAC	450
ATCGCACAAAG	AACACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	500
TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
35 TTAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
CGTCAACGTG	TTGCGTTAAC	AGGTTTAAAC	ATGGCTGAGC	ATTTCCGTGA	650
TGAGCAAGGA	CAAGATGTAC	TTCTGTTTCAT	CGATAATATC	TTCCGTTTCA	700
CGCAAGCAGG	TTCTGAAGTA	TCTGCCCTTC	TTGGCCGTAT	GCCATCTGCG	750
GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
40 TATTACATCT	ACAAATA				817

2) INFORMATION FOR SEQ ID NO: 1258

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

	CCAGAAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	TATTAACCTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTTCGTGG	CACAGAAGTA	150
10	GAAGATACTG	GTAAACCAAT	CTCTGTACCA	GTTGGTGATG	TAACACTTGG	200
	TCGCGTATTT	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAGGTTC	250
	CTGCAGATGT	ACATCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
15	CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AATTAATTAA	CAACATCGCA	450
	CAAGAGCACG	GTGGTATCTC	TGTATTCGCT	GGTGTAGGTG	AGCGTACTCG	500
	TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
20	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGCTC	GTATGCCATC	TGCGGTAGGT	750
	TACCAACCAA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATTAC	800
	ATCTACAAAT	AAAGGGTCTA	TCACGTCTA			829

25

2) INFORMATION FOR SEQ ID NO: 1259

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 844 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

	TGGCGGAAAG	CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	50
45	ACGAAAACGG	TGAACTTAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	100
	GATGATACAG	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTCTG	150
	TGGCACAGAA	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	200
	ATGCAACACT	TGGTCGCGTA	TTTAACGTAT	TAGGTGATGC	TATTGACTTA	250
	GATGGTGAGG	TTCTTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	300
50	ACCTGCATTC	GAAGAATTAT	CTACTAAAGT	AGAAATTCTT	GAAACTGGTA	350
	TTAAAGTAGT	AGACTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGC	400
	CTATTCGGTG	GTGCCGGTGT	AGGTAAACAA	GTATTAATTC	AGGAGTTAAT	450
	CAACAACATC	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	500

	GTGAGCGTAC	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	550
	GGCGTAATTA	AGAAAAGTGC	GATGGTATTC	GGACAAATGA	ACGAGCCACC	600
	TGGAGCACGT	CAACGTGTTG	CATTAACAGG	CTTAACAATG	GCTGAATATT	650
	TCCGTGATGA	GCAAGGACAA	GACGTAATTC	TGTTTCATCGA	TAATATCTTC	700
5	CGTTTCACGC	AAGCAGGTTT	TGAAGTATCT	GCCCTTCTTG	GCCGTATGCC	750
	ATCTGCGGTA	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	800
	AAGAGCGTAT	TACATCTACA	AATAAAGGGT	CTATCACGTC	TATC	844

10

2) INFORMATION FOR SEQ ID NO: 1260

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 840 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 49064

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

	AAGCTACCAG	AAATCTACAA	CGCCCTTACG	GTAAAACAGA	GCAACGAAAA	50
	CGGAACAAGC	ATTAACCTAA	CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	100
	ACACAGTTCG	TACAGTTGCA	ATGTCTTCCA	CAGATGGACT	TGTTCTGTGGC	150
30	ACAGAAGTAG	AAGATACTGG	TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	200
	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	TGATGCAATT	GACTTAGATG	250
	GTGAGGTTCC	TGCGGATGTA	CGCCGTGATC	CAATTCACCG	TCAAGCACCT	300
	GCATTCGAAG	AATTATCTAC	TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	350
	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	400
35	TCGGTGGTGC	CGGTGTAGGT	AAAACAGTAT	TAATTCAGGA	ATTAATCAAC	450
	AACATCGCAC	AAGAACACGG	TGGTATCTCT	GTATTGCTG	GTGTAGGTGA	500
	GCGTACTCGT	GAGGGTAATG	ACTTATACCA	CGAAATGAGC	GATTCAGGCG	550
	TAATTAAGAA	AAGTGCATG	GTATTCGGAC	AAATGAACGA	GCCACCTGGA	600
	GCGCGTCAAC	GTGTTGCGTT	AACAGGTTTA	ACAATGGCTG	AGCATTTCCG	650
40	TGATGAGCAA	GGACAAGACG	TTCTTCTGTT	CATCGATAAT	ATCTTCCGTT	700
	TCACGCAAGC	AGGTTCTGAA	GTATCTGCCC	TTCTTGGTCG	TATGCCATCT	750
	GCGGTAGGTT	ACCAACCAAC	ACTTGCAACA	GAAATGGGTC	AATTACAAGA	800
	GCGTATTACA	TCTACAAATA	AAGGGTCTAT	CACGTCTATC		840

45

2) INFORMATION FOR SEQ ID NO: 1261

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 839 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

10	GCGGAAAGCT	ACCAGAAATC	TACAATGCCC	TTACGGTAAA	ACAAAGCAAC	50
	GAAAACGGAA	GCATGAACTT	AACATTTGAA	GTTGCACTTC	ATTTAGGTGA	100
	TGATACAGTT	CGTACAGTTG	CGATGTCTTC	CACAGATGGA	CTTGTTTCGTG	150
	GCACAGAAGT	AGAAGATACT	GGTAAAGCAA	TCTCTGTACC	AGTTGGTGAT	200
	GCAACACTTG	GACGTGTATT	CAACGTATTA	GGTGATGCAA	TTGACTTAGA	250
15	TGGTGAAGTT	CCTGCGGATG	TACACCGTGA	TCCAATTCAC	CGTCAAGCAC	300
	CTGCATTCTGA	AGAATTATCT	ACTAAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTAGTAG	ACTTACTTGC	TCCTTACATT	AAGGGTGGTA	AGATCGGCCT	400
	ATTCGGTGGT	GCCGGCGTAG	GTAAAACAGT	ATTAATTCAG	GAGTTAATCA	450
	ATAACATCGC	ACAAGAGCAC	GGTGGTATCT	CTGTATTCTGC	TGGTGTAGGT	500
20	GAGCGTACTC	GTGAGGGTAA	TGACTTATAC	CACGAAATGA	GCGATTCTGG	550
	CGTAATCAAG	AAAAGTGC	TGGTATTCTGC	ACAAATGAAC	GAGCCACCTG	600
	GAGCACGTCA	ACGTGTTGCA	TTAACAGGTT	TAACAATGGC	TGAGCATTTT	650
	CGTGATGAGC	AAGGACAAGA	CGTACTTCTG	TTCATCGATA	ACATCTTCCG	700
	TTTCACGCAA	GCGGGTTCTG	AAGTATCTGC	CCTTCTTGGT	CGTATGCCAT	750
25	CTGCGGTAGG	TTACCAACCA	ACACTTGCAA	CAGAAATGGG	TCAATTACAA	800
	GAGCGTATTA	CATCTACAAA	TAAAGGGTCT	ATCACGTCT		839

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

45	AAGCTACCAG	AAATCTACAA	TGCCCTTACG	GTAAAACAAA	GCAACGAAAA	50
	CGGAAGCATG	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGATA	100
	CAGTTCGTAC	AGTTGCGATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
	GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
50	ACTTGACGCT	GTATTCAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
	AACTTCCTGC	GGATGTACAC	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
	TTCAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAACTG	GTATTAAAGT	350
	AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCG	400

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GTGGTGCCGG CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATCAATAAC 450
ATCGCACAAAG AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG 500
TACTCGTGAG GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA 550
TCAAGAAAAC TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA 600
5 CGTCAACGTG TTGCATTAAC AGGTTTAACA ATGGCTGAGC ATTTCCGTGA 650
TGAGCAAGGA CAAGACGTAC TTCTGTTTCAT CGATAACATC TTCCGTTTCA 700
CGCAAGCGGG TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG 750
GTAGGTTACC AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG 800
TATTACATCT ACAAATAAAG GGTCTATCAC GTC 833
10

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2) INFORMATION FOR SEQ ID NO: 1263

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
- (B) STRAIN: BGSC 4Q1

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

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CGAAAACGGA AGCATGAACT TAACATTTGA AGTTGCACTT CATTTAGGTG 50
30 ATGATACAGT TCGTACAGTT GCGATGTCTT CCACAGATGG ACTTGTTTCGT 100
GGCACAGAAG TAGAAGATAC TGGTAAAGCA ATTTCTGTAC CAGTTGGTGA 150
TGTAACACTT GGACGTGTAT TCAACGTATT AGGTGATGCA ATTGACTTAG 200
ATGGTGA ACT TCCTGCGGAT GTACACCGTG ATCCAATTCA CCGTCAAGCA 250
CCTGCATTCG AAGAATTATC TACTAAAGTA GAAATTCTTG AAAGTGGTAT 300
35 TAAAGTAGTA GACTTACTTG CTCCTTACAT TAAGGGTGGT AAGATCGGCC 350
TATTCGGTGG TGCCGGTGTA GGTAAAACAG TATTAATTCA GGAATTAATT 400
AACAAACATCG CACAAGAGCA CGGTGGTATC TCTGTATTCG CTGGTGTAGG 450
TGAGCGTACT CGTGAGGGTA ATGACTTATA CCACGAAATG AGCGATTCTG 500
GCGTAATCAA GAAAAC TGCG ATGGTATTCG GACAAATGAA CGAGCCACCT 550
40 GGAGCACGTC AACGTGTTGC ATTAACAGGT TTAACAATGG CTGAGCATTT 600
CCGTGATGAG CAAGGACAAG ACGTACTTCT GTTCATCGAT AACATCTTCC 650
GTTTCACGCA AGCGGGTTCT GAAGTATCTG CCCTTCTTGG TCGTATGCCA 700
TCTGCGGTAG GTTACCAACC AACACTTGCA ACAGAAATGG GTCAATTACA 750
AGAGCGTATT ACATCTACAA ATAAAGGGTC TATCACGTCT 790
45

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2) INFORMATION FOR SEQ ID NO: 1264

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

10

AGTTGCACTT	CATTTAGGTG	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	50
CCACAGATGG	ACTTGTCGT	GGCACAGAAG	TAGAAGATAC	TGGTAAACCA	100
ATCTCTGTAC	CAGTTGGTGA	TGTAACACTT	GGTCGCGTAT	TTAACGTATT	150
AGGTGATGCA	ATTGACTTAG	ATGGTGAGGT	TCCTGCAGAT	GTACATCGTG	200
15 ATCCAATTCA	CCGTCAAGCA	CCTGCATTTCG	AAGAATTATC	TACTAAAGTA	250
GAAATTCTTG	AAACTGGTAT	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	300
TAAGGGTGGT	AAGATCGGCC	TATTCGGTGG	TGCCGGCGTA	GGTAAACAG	350
TATTAATTCA	GGAATTAATT	AACAACATCG	CACAAGAGCA	CGGTGGTATC	400
TCTGTATTCG	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	450
20 CCACGAAATG	AGCGATTCTG	GCGTAATCAA	GAAACTGCG	ATGGTATTCG	500
GACAAATGAA	CGAGCCACCT	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	550
TTACAATGG	CTGAGCATTT	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	600
GTTTCATCGAT	AACATCTTCC	GTTTCACGCA	AGCGGGTTCT	GAAG	644

25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

GGCGGAAAGC	TACCAGAAAT	CTACAACGCC	CTTACGGTAA	AACAGAGCAA	50
CGAAAACGGA	ACAAGCATTA	ACTTAACATT	TGAAGTTGCA	CTTCATTTAG	100
45 GTGATGACAC	AGTTCGTACA	GTTGCAATGT	CTTCCACAGA	TGGACTTGTT	150
CGTGGCACAG	AAGTAGAAGA	TACTGGTAAA	GCAATCTCTG	TACCAGTTGG	200
TGATGCAACA	CTTGGTCGTG	TATTTAACGT	ATTAGGTGAT	GCAATTGACT	250
TAGATGGTGA	GGTTCCTGCG	GATGTACGTC	GTGATCCAAT	TCACCGTCAA	300
GCACCTGCAT	TCGAAGAATT	ATCTACTAAA	GTAAGAAATTC	TTGAAACTGG	350
50 TATTAAAGTA	GTAGACTTAC	TTGCTCCTTA	CATTAAGGGT	GGTAAGATCG	400
GTCTATTCGG	TGGTGCCGGT	GTAGGTAAAA	CGGTATTAAT	TCAGGAATTA	450
ATCAATAACA	TCGCACAAGA	ACACGGTGGT	ATCTCTGTAT	TCGCTGGTGT	500
AGGTGAGCGT	ACTCGTGAGG	GTAATGACTT	ATACCACGAA	ATGAGCGATT	550

	CTGGCGTAAT	TAAGAAACT	GCGATGGTAT	TCGGACAAAT	GAACGAGCCA	600
	CCTGGAGCAC	GTCAACGTGT	TGCGTTAACA	GGTTTAACAA	TGGCTGAGCA	650
	TTTCCGTGAT	GAGCAAGGAC	AAGATGTACT	TCTGTTTCATC	GATAATATCT	700
	TCCGTTTCAC	GCAAGCAGGT	TCTGAAGTAT	CTGCCCTTCT	TGGCCGTATG	750
5	CCATCTGCGG	TAGGTTACCA	ACCAACACTT	GCAACAGAAA	TGGGTCAATT	800
	ACAAGAGCGT	ATTACATCTA	CAA			823

10 2) INFORMATION FOR SEQ ID NO: 1266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

25	TGGTCCGAGR	CCCGATTCTMA	TGAAATTATC	AAGGAAACCT	CCAAYTTCAT	50
	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	CCCATTCTCTG	100
	GTTTCCAGGG	TGACAACATG	ATCGATSCCT	CTGCCAACTG	CCCATGGTAC	150
	AAGGGCTGGT	ACMAKGAGAC	TGCCGACAGG	CAAGYACTCT	GGCAAGACCC	200
30	TTCTTGAGGC	CATTGACGSC	ATTGAGCCCC	CCAMSCGTCC	TWCCGATAAA	250
	CCTCTCCGTC	TTCCTCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGMAC	300
	TGTTCTCTGTC	GGACGTRTTG	AGACTGGAGT	CATCAAGCCC	GGTATGGTCG	350
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAAATG	400
	CACCACCAGC	AGCTTTCCGA	CGGTAWCCCC	GGTGACAACG	TCGGCTTCAA	450
35	CGTCAAGAAT	GTTTCCGTCA	AAGAAGTCCG	CCGTGGTAAC	GTTGCCTGGT	500
	GACTCTAAGA	ATGATCCCGC	MAWGGGCTGC	GATTCTTCA	ATGCYCAGGT	550
	CATCGTCCTC	AACCACCCTG	GTCAGGTTGG	CGCTGGTTAT	GCCCCAGTCC	600
	TCGAYTGCCA	TACTGCCAC	ATTGCYTGCA	ARTTCGCTGA	GMTCMAGAG	650
	AAGATTGAYC	GCCGAACCGG	MAAGTCTGTT	GAGAACGCCC	CCAAGTTCAT	700
40	CAAGTCCGGT	GATGC				715

2) INFORMATION FOR SEQ ID NO: 1267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 56220

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

	GAGTCCTCTT	ATTTACTTTT	GTCATGACTA	CCTTACTAAT	CTGTCATAGA	50
	TCGTTACAAC	GAAATCGTCA	AGGAGACTTC	CAACTTCATC	AAGAAGGTCG	100
	GATACAACCC	CAAGAACGTT	CCTTTCGTTT	CTATCTCCGG	TTTCAACGGC	150
10	GACAACATGC	TTGAGCCCTC	CCCCAACTGC	CCCTGGTACA	AGGGTTGGGA	200
	GAAGGAGACC	AAGGCCGGTA	AGGTCACTGG	TAAGACCCTC	CTCGAGGCCA	250
	TCGACGCCAT	TGAGCCCCCT	ACCCGTCCCG	CCAACAAGGT	CAGTACTACC	300
	TCAATTACTT	GAAGTCTCTT	CATACGTTCC	GATTACTGAC	TGCTTCACAG	350
	CCCCCTCCGTC	TTCCCCCTCCA	GGACGTTTAC	AAGATCGGTG	GTATTGGAAC	400
15	GGTGCCCGTC	GGTCGTGTTG	AGACCGGTAC	CATCTCCCCT	GGTATGGTCG	450
	TTACCTTGTA	TGTATCCTGA	CCATCCCCCT	TGGCAATCAT	TACGTACTAA	500
	CTCACTCTTC	AGCGCTCCCG	CCAACGTCAC	CACTGAAGTC	AAGAGTGTTG	550
	AAATGCACCA	CCAGCAGCTC	GCTGCCGGTC	AGCCCGGTGA	CAACGTTGGT	600
	TTCAACGTGA	AGAACGTCTC	CGTCAAGGAA	ATCCGTCGTG	GTAACGTTGC	650
20	TGGTGATAGC	AAGAACGACC	CCCCTGCCGG	TGCTGCTTCC	TTCAACGCCC	700
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGTGCTGG	TTACGCCCCA	750
	GTCCTTGACT	GCCACACTGC	CCACATTGCT	TGCAAGTTCT	CTGAATCCT	800
	TGAGAAGATT	GACCGTCGTA	CCGGAAAGTC	TGTTGAGGAC	CACCCCAAGT	850
	TCATCAAGTC	CGGTGACGCT	GCCAT			875

2) INFORMATION FOR SEQ ID NO: 1268

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

40

(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

	GTGAGCGTGG	TATCACCATC	GATATTGCCC	TCTGGAAATT	CGAGACCCCG	50
45	AAGTACAGTG	TCACTGTCAT	TGGTGAGTGC	TTTTTACCCC	TCTTAAGCAG	100
	ATTTCAACTT	CCAGAGTATC	TACTCTAACA	TATCCGCTTA	GATGCTCCCG	150
	GCCATCGTGA	CTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	200
	TGCGCTATCC	TCATCATTGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	TCTGCTTGCT	TTCAACCTTG	300
50	GTGTGAGGCA	ACTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCCGAGTCCC	GTTTCAACGA	AATCATCAAG	GAGGTTTCCA	ACTTCATCAA	400
	GAAGGTCGGA	TATAACCCCA	AGGCTGTTCC	CTTCGTGCCA	ATCTCTGGTT	450
	TCGAGGGTGA	CAACATGATT	GAACCTCCC	CCAAGTGCAC	CTGGTACAAG	500

	GGCTGGAACA	AGGAGACTGC	CTCTGGCAAG	TCTTCTGGTA	AAACCCTTCT	550
	CGATGCCATT	GACGCCATTG	AACCCCCAAC	CCGTCCTACC	GATAAGCCTC	600
	TCCGTCTTCC	CCTCCAGGAT	GTTTACAAAA	TCTCTGGTAT	TGGCACTGTT	650
	CCCGTCGGAC	GTGTTGAGAC	TGGTGTTCATC	AAGCCCGGTA	TGGTCGTGAC	700
5	TTTCGCTCCC	TCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACCAACAAC	CCAGGCTGGT	TACCCTGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTTT	CAGTCAAGGA	AGTCCGCCGT	GGCAACGTTG	CTGGCGACTC	850
	CAAAAATGAT	CCCCCAAGG	GCTGCGAATC	CTTCAATGCC	CAGGTCATCG	900
	TCCTTAACCA	CCCCGGCCAG	GTTGGCGCTG	GTTATGCCCC	AGTCCTCGAC	950
10	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCTGAAC	TTGAGAAGAT	1000
	CGACCGCCGT	ACTGGAAAGT	CTGTTGAGAA	CAACCCCAAG	TTCATCAAGT	1050
	CTGGTGATGC	TGCTATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTG	1100
	GAGCCCTTCA	CTGACTATCC	CCCT			1124

15

2) INFORMATION FOR SEQ ID NO: 1269

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1043 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trichophyton rubrum*
- (B) STRAIN: WSA-224

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

	GTGAGCGTGG	TATCACCATC	GATATCGCCC	TCTGGAAGTT	CGAGACCCCC	50
	AAGTACAATG	TCACCGTCAT	TGGTATGTTT	CTTTGCCTTG	TTCCCTCATG	100
35	TGGTTGTACC	ATATCTAACG	AGAGTAGACG	CCCCCGGTCA	CCGTGACTTC	150
	ATCAAGAACA	TGATCACTGG	TACCTCCCAG	GCTGACTGCG	CTATTCTCAT	200
	CATTGCTGCC	GGTACTGGTG	AGTTCGAGGC	TGGTATCTCC	AAGGATGGCC	250
	AGACCCGTGA	GCACGCTCTG	CTCGCCTTCA	CCCTCGGTGT	CAAGCAGCTC	300
	ATCGTTGCCA	TCAACAAGAT	GGACACCACC	GGCTGGTCCG	AGGATCGTTT	350
40	CAAGGAAATT	ATCAAGGAAG	TCACCAACTT	CATCAAGAAG	GTTGGCTACG	400
	ACCCCAAGGG	TGTTCCATTC	GTTCCAATCT	CTGGTTTCAA	CGGTGACAAC	450
	ATGATTGAGG	CCTCCACCAA	CTGCCCATGG	TACAAGGGAT	GGAACAAGGA	500
	GACCAAGGCC	GGTGGTGCCA	AGTCCGGCAA	GACCCTCCTC	GAGGCCATCG	550
	ATGCCATCGA	CATGCCAACC	CGTCCTACCG	ACAAGCCCCT	CCGTCTCCCA	600
45	CTCCAGGATG	TCTACAAGAT	CTCTGGTATC	GGAAGTGTGC	CAGTCGGTCG	650
	TGTTGAGACC	GGTATCATCA	AGCCCGGTAT	GGTCGTCAAC	TTNGCCCCCG	700
	CCAACGTCAC	CACTGAAGTC	AAGTCCGTYK	AAATGCACCA	CCAGCAGCTT	750
	CAGCAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAATGTCA	AGAACGTTTC	800
	CGTCAAGGAA	GTCCGCCCGTG	GTAACGTTGC	CGGTGACTCC	AAGAACGACC	850
50	CACCATCCGG	CTGTGCCTCC	TTCAACGCCC	AGGTCATYGT	CCTCAACCAC	900
	CCCGGCCAGA	TCGGTGCTGG	TTACGSTCCA	GTCCTCGACT	GCCACACTGS	950
	TCACATTGCT	TGCAAGTTCG	CTGAGCTCCT	CGAGAAGATT	GACCGCCGTA	1000
	CCGGTAAATC	CGTCGAAGCC	AACCCCAAGT	TCGTCAAGTC	TGG	1043

2) INFORMATION FOR SEQ ID NO: 1270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporum canis*
 (B) STRAIN: WSA-217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

	GCTGAGCGTG	AGCGTGGTAT	CACCATTGAT	ATCGCCCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACATGGTCA	CCGTCATCGG	TATGCTTTAT	CTGTTTCCCA	100
	TTTATAGTTG	CGACCAGTAA	CTAACAAAAA	GTAGATGCCC	CCGGGCACCG	150
20	TGACTTCATC	AAGAACATGA	TTACTGGTAC	CTCCCAGGCC	GACTGCGCTA	200
	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CTCGTGAGCA	CGCCCTGCTC	GCTTTCACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	TGGTCTGAGT	350
	CCCGTTTCGG	TGAAATCATC	AAGGAAGTCA	CCAACTTCAT	CAAGAAGGTC	400
25	GGCTACGACC	CCAAGGGTGT	CCCATTCTGC	CCAATCTCTG	GCTTCAACGG	450
	TGACAACATG	ATTGAGCCCT	CCACCAACTG	CCCATGGTAC	AAGGGATGGA	500
	ACAAGGAGAC	CAAGGCCGGT	GGCAAATCCT	CTGGTAAGAC	CCTCCTTGAG	550
	GCCATCGATG	CCATTGACAT	GCCCACTCGT	CCCACCGACA	AGCCTCTCCG	600
	TCTCCCACTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	ACAGTACCAG	650
30	TCGGTCGTGT	TGAGACTGGT	ATCATCAAGC	CTGGTATGGT	TGTCACTTTY	700
	GCCCCCGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	TGCACCACCA	750
	GCAGCTYGTG	CAGGGTGTTT	CCGGTGACAA	CGTTGGCTTC	AACGTCAAGA	800
	ACGTYTCTGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	TGATTCCAAG	850
	AACGACCCAC	CAGCTGGCTG	CGCCTCTTTC	AAGGCCCAGG	TCATCGTCCT	900
35	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	CTTGACTGCC	950
	ACACTGCCCC	CATTGCTTGC	AAGTTCTCTG	AGCTTCTTGÄ	GAAGATTGAC	1000
	CGCCGTACTG	GTAAATCCGT	CGAAACCAGC	CCTAAGTTCG	TCAAGTCTGG	1050
	TGATGCCGCT	ATTGCCACCA	TGGTTCCATC	CAAGCCCATG	TGCGTTGAGG	1100
	CTTTC					1105

2) INFORMATION FOR SEQ ID NO: 1271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

5	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCTCTCTGGA	AGTTCCAGAC	50
	CCCTAAGTAT	GAGGTCACCG	TCATTGGTAT	GTTGTCCTTC	TTGTGTTACC	100
	ATCGAAACAT	ATCTAACCTA	CAACTGCAGA	CGCCCCCGGT	CACCGTGACT	150
	TCATCAAGAA	CATGATCACT	GGTACCTCCC	AGGCCGACTG	CGCTATTCTC	200
10	ATCATTGCTT	CCGGTACTGG	TGAATTCGAG	GCTGGTATCT	CCAAGGATGG	250
	CCAGACCCGT	GAGCACGCTC	TGCTCGCTTT	CACCCTCGGT	GTCCGTCAGC	300
	TCATCGTTGC	CCTCAACAAG	ATGGACACTG	CTGGCTGGGC	TGAGGCTCGT	350
	TACAACGAAA	TCGTCAAGGA	AACTTCCGGT	TTCATCAAGA	AGGTCGGCTA	400
	CAACCCCAAG	TCGGTTCCCT	TCGTCCCCAT	CTCCGGTTTC	AACGGTGACA	450
15	ACATGCTTGA	GCCCTCCTCC	AACTGCCCCCT	GGTACAAGGG	TTGGGAGAAG	500
	GAGACCAAGG	CTGGTAAGGC	CACTGGTAAG	ACCCTCCTCG	AGGCCATCGA	550
	CGCCATTGAG	CCTCCCGTCC	GTCCCTCCAA	CAAGCCTCTC	CGTCTTCCCC	600
	TCCAGGATGT	CTACAAGATC	TCTGGTATTG	GAAGTGTCCC	CGTCGGCCGT	650
	GTCGAGACCG	GTACCATCGT	CCCCGGTATG	GTCGTCACCT	TCGCTCCCGC	700
20	CAACGTCACC	ACTGAAGTCA	AGTCCGTTGA	GATGCACCAC	CAGCAGCTCA	750
	AGGAGGGTGT	TCCCGGTKAC	AACGTTGGTT	TCAACGTGAA	GAACGTTTCC	800
	GTCAAGGAAG	TCCGCCGTGG	TAACGTCGCT	GGTGACTCCA	AGAACGACCC	850
	CCCTGCCGGT	GCTGCCTCTT	TCACCGCCCA	GGTCATCGTC	CTCAACCACC	900
	CCGGTCAGGT	CGGCGCTGGT	TACGCTCCCG	TCCTCGACTG	CCACACCGCT	950
25	CACATTGCCT	GCAAGTTCGC	TGAGCTCCAG	GAGAAGATCG	ACCGCCGTAC	1000
	CGGAAAGTCT	GTCGAATYTG	CCCCCAAGTT	CATCAAGTCT	GGTGACGCCG	1050
	CTATCGTCAA	GATGATTCCC	TCCAAGCCCA	TGTGTGTCGA	GTCTTTTCACT	1100
	GACTACCCTC	CTYTCGGCCG	TTTCGCCGTC	CGTGACGTAA	GTTCTTTTCCC	1150
	CAGCTTTTCG	ATGCTACCTT	TCTMTGAATC	ACGTGTCATG	TCTTGGCACC	1200
30	CGCCCATCAC	ATGACCACGC	AACCCTATAC	CCCGCCACAC	CCTT	1244

2) INFORMATION FOR SEQ ID NO: 1272

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Exophiala moniliae*
 (B) STRAIN: WSA-219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

50	GCTGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCTCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACTATGTCA	CCGTCATCGA	CGCCCCCGGT	CATCGTGACT	100
	TCATCAAGAA	CATGATCACT	GGTACTTCCC	AAGCTGACTG	CGCCATTCTC	150
	ATCATTGCTG	CCGGTACTGG	TGAATTCGAA	GCCGGTATCT	CCAAGGATGG	200

	TCAGACCCGT	GAGCACGCTC	TGCTTGCCTA	CACCCTGGGT	GTCAAGCAGC	250
	TCATTGTCGC	CATCAACAAG	ATGGACACTA	CCAAGTGGTC	TGAGGACCGT	300
	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	AGGTCGGCTA	350
	CAACCCCAAG	TCCGTTCCCTT	TCGTCCCCAT	CTCCGGCTTC	AACGGTGACA	400
5	ACATGATCGA	CGTCTCCACC	AACTGCCCCCT	GGTACAAGGG	CTGGGAGAAG	450
	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTTG	AGGCCATCGA	500
	CGCCATTGAC	CCCCCTCTC	GTCCCACCGA	CAAGCCTYTC	CGTCTCCCTC	550
	TCCAGGATGT	GTACAAGATC	TCTGGTATCG	GAACGGTGCC	CGTCGGTCGT	600
	GTCGAGACTG	GTATCATCAA	GGCCGGTATG	GTCGTTACCT	TCGCTCCTGC	650
10	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	GAACAGCTCG	700
	CCGAGGGTGT	TCCAGGTGAC	AACGTCGGTT	TCAACGTCAA	GAACGTYTCC	750
	GTCAAGGAGG	TTCGTCGTGG	AAACGTTTGC	GGTGACTCCA	AGAACGACCC	800
	ACCCAAGGGC	GCTGATTCCT	TCAACGCCCA	GGTCATCGTC	TTGAACCACC	850
	CTGGTCAAGT	TGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	CCACACTGCC	900
15	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATCG	ATCGTCGKAC	950
	CGGAAAGTCG	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	GGTGACGCTG	1000
	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TG		1032

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2) INFORMATION FOR SEQ ID NO: 1273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*
 (B) STRAIN: ATCC 34944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

	TAACAGCCCCG	TGCGACCGTC	TCGTCCAATA	ACTAATGATT	CGCAGGTACT	50
	ATGTCGTGAG	TATCCGGTCC	TTTTTTGTTA	ATTTACCAGA	AATGACGAAA	100
	TTTTTGACTA	ATTAACACAC	TCAGACCGTC	ATTGACGCC	CGGGTCACCG	150
40	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCC	GACTGCGCTG	200
	TCCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTCGCCATCA	ATAAGATGGA	CACCACCAAG	TGGTCCGAGG	350
	AGCGTTACGG	CGAGATCATC	AAGGAGACCT	CTGCCTTCAT	CAAGAAGGTC	400
45	GGTTTCAACC	CGAAGCACGT	CCCGTTCTGC	CCGATCTCCG	GTTTCAACGG	450
	TGACAACATG	ATCGAGGCCT	YACCAACTG	CCCGTGGTAC	AAGGGCTGGG	500
	AGAAGGAGAC	CAAGGCCAAG	GTCACCGGCA	AGACCCTYCT	TGAGGCCATT	550
	GACAACATCG	ACCCGCCGAG	CCGTCCTTCC	GACAAGCCGC	TCCGTCTTCC	600
	CCTCCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGGACAGTC	CCAGTCGGCC	650
50	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTTAC	CTTCGCTCCG	700
	GCTGGTGTCA	CCACTGAAGT	GAAGTCCGTT	GARATGCACC	ACGAGCAGCT	750
	CGCTGAGGGT	YTGCCGGGTG	ACAACGTCGG	CTTCAACGTC	AAGAACGTTT	800
	CCGTCAAGGA	GATCCGTCGT	GGCAACGTTG	CTGGTGACAG	CAAGGCTGAC	850

	CCGCCGAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	TCCTGAACCA	900
	CCCTGGCCAG	GTCGGTGCTG	GTTACGCTCC	AGTCCTGGAC	TGCCACACTG	950
	CCCACATTGC	CTGCAAGTTC	GGCGAGCTCC	TCGAGAAGAT	CGACCGTCGC	1000
	TYTGGCAAGT	CCATTGAAGC	CTYGCCTAAG	TACATCAAGT	CTGGTGACGC	1050
5	TGCCATYGTC	AAGATGATTC	CGTCCAAGCC	GATGTGCGTT	GAGCCATTCA	1100
	CTGAGT					1106

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
 (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

25	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTTCGAGACT	CCCCGCTACT	ATGTCACCGT	CATTGGTATG	TTGCTGTCAC	100
	CTCTCTCACA	CATGTCTCAC	CACTAACAAT	CAACAGACGC	CCCCGGCCAC	150
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGACTGCGC	200
30	CATTCTCATC	ATTGCCGCCG	GTACTGGTGA	GTTTCGAGGCT	GGTATCTCCA	250
	AGGATGGCCA	GACCCGTGAG	CACGCCCTGC	TCGCCTACAC	CCTCGGTGTC	300
	AAGAACCTCA	TTGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	350
	GTCCCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAACCTC	ATCAAGAAGG	400
	TCGGCTACAA	CCCCAAGGCT	GTCGCTTTTCG	TCCCCATCTC	CGGTTTCAAC	450
35	GGCGACAACA	TGCTTACTCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGCTG	500
	GGAGCGTGAG	ATCAAGTCCG	GCAAGCTCAC	TGGCAAGACC	CTCCTCGAGG	550
	CCATTGACTC	CATCGAGCCC	CCCAAGCGTC	CCGTCGACAA	GCCCCTYCGA	600
	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATTGGCA	CGGTTCCCGT	650
	CGGCCGTATC	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTMG	700
40	CCCCCTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	750
	CAGCTCTYTG	AGGGTCTTCC	CGGTGACAAC	GTCGGCTTCA	ACGTGAAGAA	800
	CGTYTCCGTC	AAGGAGATCC	GACGTGGCAA	CGTCGCTGGT	GACTCCAAGA	850
	ACGACCCCCC	TYTGGGTGCC	GCCTCTTTCA	CCGCCCAGGT	CATTGTCCTC	900
	AACCACCCTG	GCCAGGTCGG	TGCCGGTTAC	GCCCCCGTTY	TGGACTGCCA	950
45	CACTGCCCCAC	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	1000
	GCCGAAGTGG	TAAGGCTGTT	GAGTCCGCCC	CCAAGTTCAT	CAAGTCTGGT	1050
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1100
	TTTCACTGAC	TACCCCCCT				1119

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2) INFORMATION FOR SEQ ID NO: 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

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15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGACTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC T GCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTGAGGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGA CTCCAAGAACGA      800
   CCCCCCAAG GGTGTGACT CCTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTGCGGTGCT GGTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG      1000
35 CCGCCATCGT CAAGATGGTT CCCTCCAAGC CCATGTGTGT TGAGGCTTTC      1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113

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2) INFORMATION FOR SEQ ID NO: 1276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

	GGTCTGAGAC	CCGTTTCAAC	GAAATTATCA	AGGAAGTCAG	CAACTTCATC	50
5	AAGAAGGTCG	GATACAACCC	CAAGTCTGTT	CCCTTCGTGC	CAATCTCCGG	100
	TTTCGAGGGT	GACAACATGA	TTGAGCCTTC	CCCCAACTGC	CCTTGGTACA	150
	AGGGCTGGAA	CAAGGAGACT	GCTGCTGGCA	AGGCCGCCGG	TAAGACTCTT	200
	CTCGATGCCA	TTGACGCCAT	CGACCCCCCC	GTCCGTCCTA	CCGAGAAGCC	250
	TCTCCGTCTT	CCCCTCCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	300
10	TTCCC GTTGG	ACGTGTCGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTG	350
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TTGAAATGCA	400
	CCACCAGCAG	CTCCAGGCTG	GTTACCCTGG	TGACAACGTC	GGCTTCAACG	450
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCGGTGAC	500
	TCCAAGAACG	ACCCCCCAA	GGGCTGCGAG	TCCTTCAACG	CCCAGGTCAT	550
15	CGTCCTCAAC	CACCCCGGCC	AGGTGCGCGC	TGGTTATGCC	CCAGTCCTCG	600
	ACTGCCACAC	TGCCACATT	GCTTGCAAGT	TCTCTGAGCT	CATCGAGAAG	650
	ATTGACCGCC	GTACCGGAAA	GTCTGTTGAG	GACAACCCCA	AGTTCATCAA	700
	GTCCGGTGAT	GCTGCTATCG	TCAAGATGAT	T		731

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2) INFORMATION FOR SEQ ID NO: 1277

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1046 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exophiala dermatitidis*
 (B) STRAIN: ATCC 76088

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCCCTCTG	GAAGTTCGAG	50
	ACCCCCAAGT	ACTATGTCAC	CGTCATCGAC	GCCCCGGGTC	ATCGTGACTT	100
40	TATCAAGAAC	ATGATCACTG	GTACCTCGCA	GGCCGACTGC	GCCATCTTGA	150
	TCATTGCCGC	CGGTACCGGT	GAATTCTGAAG	CCGGTATCTC	CAAGGATGGT	200
	CAGACCCGTG	AGCACGCTCT	GCTCGCCTAC	ACCTTGGGTG	TCAAGCAGCT	250
	CATCGTCGCC	ATCAACAAGA	TGGACACCAC	CAAGTGGTCC	GAGGAGCGTT	300
	TCAACGAAAT	CATCAAGGAG	ACTTCCAAC	TCATCAAGAA	GGTCGGCTAC	350
45	AACCCCAAGG	CCGTTCCTTT	CGTCCCCATC	TCCGGCTTCA	ACGGTGACAA	400
	CATGATTGAG	GTCTCCACCA	ACTGCCCGTG	GTACAAGGGA	TGGGAGAAGG	450
	AGTCCAAGGC	TGGCAAGGCC	ACCGGCAAGA	CCCTCCTCGA	GGCCATTGAC	500
	GCCATCGACC	CACCCACCCG	TCCCACCGAC	AAGCCTCTCC	GTCTCCCTCT	550
	CCAGGATGTC	TACAAGATCT	CTGGTATCGG	AACGGTTCCT	GTCGGTCGTG	600
50	TCGAGACCGG	TACCATCAAG	GCCGGTATGG	TCGTACCTT	CGCTCCGGCC	650
	AACGTCACCA	CTGAAGTCAA	GTCCGTCGAA	ATGCACCACG	AGCAGCTCGC	700
	CGAGGGTYTG	CCAGGTGACA	ACGTTGGCTT	CAACGTCAAG	AACGTYTCCG	750
	TCAAGGAGGT	TCGTCTGGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCG	800

	CCCAAGGGTG	CCGAGTCCTT	CAACGCCCAG	GTCATTGTCC	TCAACCACCC	850
	TGGTCAGATC	GGTGCCGGCT	ACGCTCCAGT	CTTGGATTGC	CACACTGCCC	900
	ACATTGCTTG	CAAGTTCGCC	GAGTTGCTCG	AGAAGATCGA	CCGTCGTACC	950
	GGAAAGTCCA	TCGAGAACAA	CCCCAAGTTC	ATCAAGTCTG	GTGATGCTGC	1000
5	CATCGTCAAG	ATGATTCCCA	GCAAGCCCAT	GTGTGTCGAG	GCTTTC	1046

2) INFORMATION FOR SEQ ID NO: 1278

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
 (B) STRAIN: WSA-213

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

25	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	TCGAGACTCC	50
	TCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GTCGCTCATA	CCTCATCCTA	100
	CTTCCTCATA	CTAACACATC	ATTCAGACGC	TCCCGGTAC	CGTGATTTC	150
	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGATTGCGC	CATTCTCATC	200
	ATTGCCGCCG	GTA CTGGTGA	GTTTCGAGGCT	GGTATCTCCA	AGGATGGCCA	250
30	GACCCGTGAG	CACGCTCTTC	TTGCCTACAC	CCTTGGTGTC	AAGAACCTCA	300
	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCTGA	GGCCCGTTAC	350
	CAGGAGATCA	TCAAGGAGAC	CTCCTCTTTC	ATCAAGAAGG	TCGGCTACAA	400
	CCCCAAGGCT	GTCGCTTTTCG	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	450
	TGCTTACCCC	CTCCACCAAC	TGCCCCTGGT	ACAAGGGTTG	GGAGCGTGAG	500
35	ATCAAGTCCG	GCAAGCTCTC	CGGCAAGACC	CTCCTCGAGG	CCATTGACTC	550
	CATCGAGCCT	CCCAAGCGTC	CCGTTGACAA	GCCCCCTCCG	CTTCCCCCTCC	600
	AGGATGTCTA	CAAGATCGGT	GGTATTGGAA	CGGTTCCCGT	CGGCCGTATT	650
	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTCG	CTCCCTCCAA	700
	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	CAGYTCAGTK	750
40	AGGGCCAGCC	CGGTGACAAC	GTTGGTTTCA	ACGTGAAGAA	CGTTTCCGTC	800
	AAGGACATCC	GACGTGGTAA	CGTCGCTGGT	GACTCCAAGA	ACGACCCCCC	850
	CCAGGGTGCC	GCTTCTTTCA	CCGCCAGGT	CATCGTCCTC	AACCACCCCG	900
	GCCAGGTCGG	TGCTGGTTAC	GCTCCTGTCC	TCGATTGCCA	CACTGCCCAC	950
	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	GCCGAACCGG	1000
45	TAAGGCTACT	GAGGCCGCTC	CCAAGTTCAT	CAAGTCTGGT	GACTCCGCCA	1050
	TCGTCAAGAT	GGTTCCTCC	AAGCCCATGT	GTGTCGAGGC	TTTCACTGAC	1100
	TACCCTCCT					1109

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2) INFORMATION FOR SEQ ID NO: 1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*
- (B) STRAIN: WSA-174

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

	CCTGCAAGTG	GTCTGAGGAC	CGTTACAACG	AAATCGTGAA	GGAGACCTCC	50
15	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	100
	CATCTCCGGT	TTCAACGGTG	ACAACATGCT	TGAGCCTTCC	CCCAACTGCC	150
	CCTGGTACAA	GGGTGAGGAG	AAGGAGGGCA	AGTCCGGCAA	GGTCACCGGT	200
	AAGACTCTCC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCGG	TCCGTCTCTGC	250
	CAACAAGCCT	CTCCGTCTTC	CCCTCCAGGA	TGTGTACAAG	ATCTCTGGTA	300
20	TCGGAAGTGT	CCCCGTTCGGC	CGTGTGCGAG	CTGGTGTTCAT	CACCCCCGGC	350
	ATGGTTGTTA	CCTTCGCTCC	TTCCAACGTC	ACCACTGAAG	TGAAGTCCGT	400
	TGAGATGCAC	CACCAGCAGC	TCAAGGAGGG	TCTCCCCGGT	GACAACGTTG	450
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AGGTCCGTCG	TGGTAACGTC	500
	GCTGGTGACT	CCAAGAACGA	CCCCCTGCT	GGCGCTGCCT	CCTTCACCGC	550
25	CCAGGTCATC	GTTCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGCTACGCCC	600
	CCGTCTCGA	CTGCCACACT	GCCCACATTG	CCTGCAAGTT	CGCTGAGCTC	650
	CAGGAGAAGA	TTGACCGCCG	TACCGGAAAG	TCTGTTGAGT	CTTCTCCCAA	700
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATC	CCTYCAAAGC	750
	CCATGTGCGT	CGAAG				765

30

2) INFORMATION FOR SEQ ID NO: 1280

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 64746

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	GAAGTTCCAG	ACTCCCAAGT	50
50	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	CGCCCCGATA	TGTTTTGGTG	100
	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	150
	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	CTGCGCTATC	CTCATCATTTG	200
	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	TCTCCAAGGA	TGGCCAGACC	250

	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	GGTGTCAAGC	AGCTCATCGT	300
	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	GTCCGAGGAT	CGTTACAACG	350
	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	400
	AAGGCCGTTT	CCTTCGTMCC	CATCKCTGGC	TTCAACGGTG	ACAACATGCT	450
5	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	GGGATGGGAG	AAGGAGACCA	500
	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	TCGAGGCCAT	YGACGCCATT	550
	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	CTYCGTCTTC	CCCTCCAGGA	600
	TGTYTACAAG	ATCTCTGGTA	TCGGAACGGT	CCCTGTCTGGC	CGTGTCGAGA	650
	CCGGTATCAT	CAAGCCC GGC	ATGGTCGTCA	CCTTTGCCCC	CGCCAACGTC	700
10	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	CACCAGCAGC	TCCAGGAGGG	750
	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	CAAGAACGTT	TCCGTCAAGG	800
	AAGTCCSCCG	TGGTAACGTT	TGCGGTGACT	CCAAGAACGA	TCCCCCTCAG	850
	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	GTCTCTCAAC	ACCCCGGTCA	900
	GGTCGGCGCT	GGTTACGCC	CCGTCCTCGA	CTGCCACACT	GCCACATTG	950
15	CTTGCAAGTT	CTYTGAGCTG	CTTGAGAAGA	TTGACCGCCG	TACCGGCAAG	1000
	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	TCCGGTGAWG	CCGCCATCGT	1050
	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	CGAGTCCTTC	ACTGACTACC	1100
	CCCCT					1105

20

2) INFORMATION FOR SEQ ID NO: 1281

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 1343 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus laurentii*
(B) STRAIN: ATCC 44096
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

	GCCGAGCGAG	AGCGAGGTAT	CACCATCGAC	ATTGCTCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACAACGTCA	CCGTCAATTGA	CGCCCCCGGA	CACCGAGACT	100
40	TCATCAAGAA	CATGATCACC	GGTACCTCCC	AGGCCGACTG	CGCCATCCTT	150
	ATCATTGCCA	CCGGTATCGG	AGAGTTCGAG	GCCGGTATCT	CTAAGGACGG	200
	TCAGACCCGA	GAGCACGCTT	TGCTCGCCTT	CACCCTCGGT	GTCAGGCAGC	250
	TCATCGTTGC	TTGCAACAAG	ATGGACACCT	GCAAGTGGTC	CGAGGACCGA	300
	TTCAACGAGA	TCGTCAAGGA	GACCAACGGT	TTCATCAAGA	AGGTCGGATA	350
45	CAACCCCAAG	GCTGTTCCCT	TCGTCCCCAT	CTCTGGATGG	CACGGAGACA	400
	AGTGAGTGCC	GTTCTTTGCG	TTGAGCCCTC	TTTGTCGCTC	CCCCTCCCTC	450
	TCAAGTGGCG	GCGGCGGTCT	CCACCCACAA	ATCGGGTGGC	GAATCCGCCA	500
	CACCCACCAC	TTCTCGCCAC	CGAGTGTGGC	ACTTCTTCCA	ACTCCTCTTT	550
	CCACTCCTCC	TCGTCTCGTC	TCTTTTTTTC	TCCGTTGTCT	TTGACAAGGG	600
50	GAGTGTGCTG	ATAGTAAAGC	ATGCTTGAGG	AGACCACCAA	CATGCCGTGG	650
	TACAAGGGAT	GGACCAAGGA	GACCAAGTCC	GGTGTCTGTTA	AGGGTAAGAC	700
	CCTCCTCGAC	GCCATCGACG	CCATCGAGCC	TCCTCAACGA	CCCACCGACA	750
	AGCCCTCCG	ACTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATCGGT	800

	ACGGTGCCCCG	TCGGCCGAGT	CGAGACCGGT	GTCATCAAGG	CCGGGTAAAGT	850
	CACGGGAGCC	TGACGGCTGT	TGTTGCCACA	CCCAACTTAT	ATCCAGTATG	900
	GTCGTCACCT	TCGCTCCTAC	CAACGTCACC	ACTGAGGTTA	AGTCCGTTGA	950
	GATGCACCAC	GAGCAGATCC	CTGAGGGTCT	TCCCGGAGAC	AACGTTGGTT	1000
5	TCAACGTGAA	GAACGTTTCC	ATCAAGGACA	TCCGACGAGG	AAACGTYTGC	1050
	TCCGACTCCA	AGAACGACCC	CGCTAAGGAG	GCCGCTTCTT	TCAACGCCCCA	1100
	GGTCATTGTC	CTCAACCACC	CTGGACAGAT	TGGTGCCGGT	TACACCCCCG	1150
	TCCTCGACTG	CCACACCGCC	CACATTGCCT	GCAAGTTCGC	CGAGCTCATC	1200
	GAGAAGATCG	ACCGACGAAC	TGGTAAGACC	ATGGAGGCCG	CCCCCAAGTT	1250
10	CGTCAAGTCC	GGAGACGCCG	CCATTGTCAA	GCTCGTTGCC	CAGAAGCCCCA	1300
	TCTGTGTCGA	GTCTTACTCT	GACTACCCTC	CCCTTGACG	ATT	1343

15 2) INFORMATION FOR SEQ ID NO: 1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

30	TGGTCCGAGG	CTCGTTTCAA	CGAAATCATC	AAGGAAGTCA	CCAAC TTCAT	50
	CAAGAAGGTC	GGATAACAAC	CCAAGTCTGT	TCCCTTCGTG	CCAATCTCTG	100
	GTTTCGAGGG	TGATAACATG	ATTGAGCCCT	CCACCAACTG	CCCCTGGTAC	150
	AAGGGCTGGA	CCAAGGAGAC	CGTGCCGGC	AAGTCAACCG	GTAAGACTCT	200
35	TCTTGACGCC	ATTGATGCCA	TCGATCAACC	CTCCCGTCCT	ACCGACAAGC	250
	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AGATCTCCGG	TATTGGCACT	300
	GTTCCCGTTG	GACGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTCGT	350
	GACCTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	400
	ACCACCAACA	GCTCTTGGCT	GGTAACCCCG	GTGACAACGT	CGGTTTCAAC	450
40	GTCAAGAACG	TTTCCGTCAA	GGAAGTCCGC	CGTGGCAACG	TTGCTGGTGA	500
	CTCAAAGAAC	GACCCCCCCA	AGGGCTGCGA	CTCCTTCAAC	GCCCAGGTCA	550
	TCGTCCTCAA	TCACCCCGGT	CAAGTTGGCG	CTGGTTATGC	CCCAGTCCTC	600
	GACTGCCACA	CTGCCACAT	TGCTTGCAAG	TTCTCTGAGC	TCCTCGAGAA	650
	GATTGACCGC	CGTACCGGAA	AGTCCACTGA	GAACAACCCC	AAGTTCATCA	700
45	AGTCTGGTGA	CGCCGCTATC	GTCAAGATGG	TTCC		734

2) INFORMATION FOR SEQ ID NO: 1283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

	CGTGAGCGTG	GATCACCAT	CGACATTGCC	CTCTGGAAGT	TCGAGACTCC	50
	CCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GCTGTCACCT	CTCTCACACA	100
	TGTCTCACCA	CTAACAATCA	ACAGACGCC	CCGGCCACCG	TGACTTCATC	150
15	AAGAACATGA	TCACTGGTAC	TTCCCAGGCC	GACTGCGCCA	TTCTCATCAT	200
	TGCCGCTGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	250
	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GAACCTCATT	300
	GTCGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTACCA	350
	GGAGATCATC	AAGGAGACCT	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	400
20	CCAAGGCTGT	CGCTTTCGTC	CCCATCTCCG	GTTTCAACGG	CGACAACATG	450
	CTTACTCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGCTGGG	AGCGTGAGAT	500
	CAAGTCCGGC	AAGCTCACTG	GCAAGACCCT	CCTCGAGGCC	ATTGACTCCA	550
	TCGAGCCCCC	CAAGCGTCCC	GTCGACAAGC	CCCTCCGACT	TCCCCTCCAG	600
	GATGTCTACA	AGATCGGTGG	TATTGGCACG	GTTCCCGTCG	GCCGTATCGA	650
25	GACTGGTGTG	ATCAAGCCCC	GTATGGTCGT	TACCTTCGCC	CCCTCCAACG	700
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTCTYTGAG	750
	GGTCTTCCCC	GTGACAACGT	CGGCTTCAAC	GTKAAGAACG	TYTCCGTCAA	800
	GGAGATCCGA	CGTGGCAACG	TCGCTGGTGA	CTCCAAGAAC	GACCCCCCTY	850
	TGGGTGCCGC	CTCTTTCACC	GCCCAGGTCA	TTGTCCTCAA	CCACCCTGGC	900
30	CAGGTCGGTG	CCGGTTACGC	CCCCGTTYTG	GACTGCCACA	CTGCCACAT	950
	TGCCTGCAAG	TTCGCCGAGA	TCCAGGAGAA	GATCGACCGC	CGAACTGGTA	1000
	AGGCTGTTGA	GTCCGCCCCC	AAGTTCATCA	AGTCTGGTGA	CTCCGCCATC	1050
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACTGACTA	1100
	CCCCCCT					1107

35

2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: ATCC 14285

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

	GCTCAAGGCC	GAGCGTGAGC	GCGGTATCAC	CATCGATATT	GCTCTGTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TACGTCACCG	TCATTGACGC	CCCCGGTCAT	100
	CGCGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTCGAGGCT	GGTATCTCCA	200
5	AGGATGGCCA	GACTCGTGAG	CACGCTCTGC	TCGCCTACAC	CCTGGGTGTG	250
	CGGCAGCTGA	TCGTGCGCCAT	CAACAAGATG	GACACGGCCA	AGTGGGCTGA	300
	GGCTCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAAC TTC	ATCAAGAAGG	350
	TCGGCTACAA	CCCCAAGACT	GTTGCCTTCG	TCCCCATCTC	GGGCTTCCAC	400
	GGCGACAACA	TGCTTACTCC	CTCGACCAAC	TGCCCCCTGGT	ACAAGGGCTG	450
10	GGAGAAGGAG	GGCAAGAGCG	GCAAGGTTAC	CGGTAAGACT	CTGCTGGACG	500
	CCATTGACGC	CGTCGAGCCC	CCCAAGCGCC	CCACGGACAA	GCCCCTGCGT	550
	CTGCCCCTCC	AGGATGTCTA	CAAGATCGGC	GGTATCGGCA	CTGTCCCTGT	600
	CGGCCGTATC	GAGACTGGTG	TCCTGAAGCC	CGGCATGGTC	GTCACCTTTG	650
	CCCCGTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
15	CAGCTTGTTG	AGGGTGTTCC	CGGCGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
	CGTYTCCGTC	AAGGAGATCC	GTGTTGGCAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCCCC	CTCGGGCGCC	GCCACCTTCA	ACGCCCAGGT	CATTGTCCTG	850
	AACCACCCCCG	GCCAGGTCGG	CAACGGCTAC	GCCCCGGTTY	TGGACTGCCA	900
	CACCGCCCCAC	ATTGCCTGCA	AGTTCACCGA	GATCCTTGAG	AAGATCGACC	950
20	GCCGTACCGG	CAAGTCGGTT	GAGAACAACC	CCAAGTTCAT	CAAGTCGGGT	1000
	GACGCCGCCA	TTGTCAAGCT	GACGCCCTYG	AAGCCCATGT	GCGTT	1045

25 2) INFORMATION FOR SEQ ID NO: 1285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

40	TTGCCAGTGG	TCCGAGGCC	GTTACAACGA	AATCGTCAAG	GAGACTTCCG	50
	GTTTCATCAA	GAAGGTCGGA	TACAACCCCA	AGTCCGTTGC	CTTCGTCCCC	100
	ATCTCCGGTT	TCAACGGTGA	CAACATGCTC	GAGGCCTCTA	CCAACTGCCC	150
	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	GGCCGGTAAG	GCCACTGGTA	200
45	AGACCCTCCT	TGAGGCCATC	GACGCCATTG	AGCCCCCCAC	CCGTCCCTCC	250
	AACAAGCCCC	TCCGTCTTCC	CCTCCAGGAT	GTCTACAAGA	TCTCCGGTAT	300
	TGGAAGTGTG	CCCGTCGGCC	GTGTCGAGAC	TGGTGTTATC	ACCCCCGGCA	350
	TGGTCGTCAC	CTTCGCTCCT	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTT	400
	GAGATGCACC	ACCAGCAGCT	CAAGGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
50	TTTCAACGTC	AAGAACGTTT	CCGTCAAGGA	AATCCGTCGT	GGTAACGTTG	500
	CCTCCGACTC	CAAGAACGAC	CCCGCCTCCG	GCGCTGCCTC	TTTCAACGCC	550
	CAGGTCATCG	TTCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	600
	CGTCCTCGAC	TGCCACACCG	CCCACATTGC	TTGCAAGTTC	TCTGAGCTTC	650

TTGAGAAGAT	TGACCGCCGT	ACCGGAAAGG	CTGTTGAAAC	CAGCCCCAAG	700
TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	CTTCCAAGCC	750
CATGTGCGKT	CCGA				764

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2) INFORMATION FOR SEQ ID NO: 1286

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 971 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 16264

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

ACCATCGATA	TCGCGCTCTG	GAAGTTCGAG	ACTCCCAAGT	ACTTCGTCAC	50
CGTCATCGAT	GCCCCTGGTC	ATCGTGACTT	CATCAAGAAC	ATGATCACTG	100
25 GTACCTCCCA	GGCTGATTGT	GCTATTCTCA	TCATTGCCGC	TGGTACTGGT	150
GAGTTCGAGG	CCGGTATCTC	CAAGGATGGC	CAGACCCGTG	AGCATGCTCT	200
GCTCGCCTAC	ACCCTGGGCG	TGAAGCAGCT	TATCGTCGCC	ATCAACAAGA	250
TGGACACCAC	CAAATGGTCT	GAGGATCGTT	TCAACGAAAT	CATCAAGGAG	300
ACTTCCAAC	TCATCAAGAA	GGTCGGATAC	AACCCCAAGT	CCGTTCCATT	350
30 CGTGCCCATC	TCCGGCTTCA	ACGGTGACAA	CATGATCGAC	GTCTCCACCA	400
ATGCCCCCTG	GTACAAGGGC	TGGGAAAAGG	AGTCCAAGGC	TGGCAAGGCC	450
ACCGGCAAGA	CCCTCCTTGA	GGCTATCGAC	TCCATCGACC	CTCCTGCTCG	500
TCCCACCGAC	AAGCCTCTCC	GTCTCCCACT	CCAGGATGTC	TACAAGATTT	550
CTGGTATCGG	CACGGTGCCC	GTCGGTCGTG	TTGAGACTGG	TACCATCAAG	600
35 GCCGGTATGG	TCGTCACCTT	TGCCCCCGCC	AACGTCACCA	CTGAAGTCAA	650
GTCCGTCGAA	ATGCACCACG	AACAGCTYGC	CGAGGGCGTT	CCGGGTGACA	700
ACGTCGGCTT	CAACGTCAAG	AACGTYTCCG	TGAAGGAGGT	TCGTCGTGGA	750
AACGTTGCTG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTG	CCGACTCCTT	800
CAACGCCCCAG	GTCATCGTCC	TCAACCACCC	TGGTCAGGTC	GGTGCTGGCT	850
40 ACGCCCCGGT	CTTGGATTGC	CACACTGCC	ACATTGCCTG	CAAGTTCTYT	900
GAGCTCCTCG	AGAAGATCGA	TCGTCGKACC	GGCAAGTCCA	TGGAAAACAA	950
CCCCAAGTTC	ATCAAGTCTG	G			971

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2) INFORMATION FOR SEQ ID NO: 1287

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exserohilum rostratum*

(B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

	GGTCTGAGGA	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	50
10	AAGAAGGTCG	GCTACAACCC	CAAGCACGTT	CCCTTCGTCC	CCATCTCCGG	100
	TTTCAACGGA	GACAACATGA	TCGAGGCCTC	CAGCAACTGC	CCCTGGTACA	150
	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACTGGTAA	GACCCTCCTT	200
	GAGGCCATTG	ACGCCATCGA	CCCTCCCAGC	CGTCCTACCG	ACAAGCCCCT	250
	CCGTCTTCCC	CTCCAGGATG	TCTACAAGAT	TGGTGGTATT	GGCACGGTTC	300
15	CCGTCGGTTCG	TGTCGAGACC	GGTATCATCA	AGGCCGGTAT	GGTCGTCACC	350
	TTCGCCCCCG	CTGGTGTGAC	CACTGAAGTC	AAGTCCGTCG	AGATGCACCA	400
	CGAGCAGCTT	ACCGAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAACGTCA	450
	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GTAACGTTGC	CGGTGACTCC	500
	AAGAACGACC	CCCCCAAGGG	CTGCGAGTCT	TTCAACGCTC	AGGTCATTGT	550
20	CCTCAACCAC	CCTGGTCAGG	TCGGTGCCGG	TTACGCGCCA	GTCCTCGACT	600
	GCCACACCGC	CCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	CGAGAAGATT	650
	GACCGCCGTA	CCGGAAAGTC	TGTCGAAGCC	TCTCCCAAGT	TCATCAAGTC	700
	TGGTGACGCG	GCCATCGTCA	AGATGGTTCC	CT		732

25

2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1236

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

	AATGGATCCT	GTATACGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTRC	50
	TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTGGAAAT	CGCGGAAGCA	100
45	CTTGTACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
	TCTTGTACCG	AAAGCAGAGA	TTGAAGGCGA	TATGGGTGAC	TCACACGTAG	200
	GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTMGTAAGCT	TTCAGGAGCA	250
	ATCAACAAAT	CARRARCAAT	WGCAATCTTT	ATTAACCAAA	TTCGWGAAAA	300
	AGTTGGGGTT	ATGTTTCGGAA	ACCCAGAAAC	AACTCCA		337

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2) INFORMATION FOR SEQ ID NO: 1289

700

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

AATGGATCCT	GTATATGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTTC	50
TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTGGAAAT	CGCGGAAGCA	100
CTTGTACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
TCTTGTACCG	AAAGCAGAGA	TTGAAGGCGA	TATGGGTGAC	TCACACGTAG	200
GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTMGTAAGCT	TTCAGGAGCA	250
ATCAACAAAT	CARAARCAAT	TGCAATCTTT	ATTAACCAA	TTCGTGAAAA	300
AGTTGGGGTT	ATGTTTCGAA	ACCCAGAAAC	AACTCC		336

2) INFORMATION FOR SEQ ID NO: 1290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT

23

2) INFORMATION FOR SEQ ID NO: 1291

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

GCIYTTICCIG AYGTIMGIGA YGG

23

5 2) INFORMATION FOR SEQ ID NO: 1292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

ARISCYTCIA RIATRTGIGC

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2) INFORMATION FOR SEQ ID NO: 1293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

ATGGCTGAAT TACCTCAATC

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2) INFORMATION FOR SEQ ID NO: 1294

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

ATGATTGTTG TATATCTTCT TCAAC

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2) INFORMATION FOR SEQ ID NO: 1295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295

CAGAAAGTTT GAAGCGTTGT

2) INFORMATION FOR SEQ ID NO: 1296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296

AACGATTCGT GAGTCAGATA

2) INFORMATION FOR SEQ ID NO: 1297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297

CGGTCAACAT TGAGGAAGAG CT

2) INFORMATION FOR SEQ ID NO: 1298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

ACGAAATCGA CCGTCTCTTT TTC

23

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2711 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: 601055
- (C) ACCESSION NUMBER: X71437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

	ATGGCTGAAT	TACCTCAATC	AAGAATAAAT	GAACGAAATA	TTACCAGTGA	50
	AATGCGTGAA	TCATTTTTAG	ATTATGCGAT	GAGTGTATC	GTTGCTCGTG	100
30	CATTGCCAGA	TGTTCTGTGAC	GGTTTAAAAC	CAGTACATCG	TCGTATACTA	150
	TATGGATTAA	ATGAACAAGG	TATGACACCG	GATAAATCAT	ATAAAAAATC	200
	AGCACGTATC	GTTGGTGACG	TAATGGGTAA	ATATCACCT	CATGGTGACT	250
	CATCTATTTA	TGAAGCAATG	GTACGTATGG	CTCAAGATTT	CAGTTATCGT	300
	TATCCGCTTG	TTGATGGCCA	AGGTAACCTT	GGTTCAATGG	ATGGAGATGG	350
35	CGCAGCAGCA	ATGCGTTATA	CTGAAGCGCG	TATGACTAAA	ATCACACTTG	400
	AACTGTTACG	TGATATTAAT	AAAGATACAA	TAGATTTTAT	CGATAACTAT	450
	GATGGTAATG	AAAGAGAGCC	GTCAGTCTTA	CCTGCTCGAT	TCCCTAATTT	500
	ATTAGCCAAT	GGTGCATCAG	GTATCGCGGT	AGGTATGGCA	ACGAATATTC	550
	CACCACATAA	CTTAACAGAA	TTAATCAATG	GTGTAAGTAA	CTTAAGTAAG	600
40	AACCCTGATA	TTTCAATTGC	TGAGTTAATG	GAAGATATTG	AAGGTCCTGA	650
	TTTCCCAACT	GCTGGACTTA	TTTTAGGTAA	GAGTGGTATT	AGACGTGCAT	700
	ATGAAACAGG	TCGTGGTTCA	ATTCAAATGC	GTTCTCGTGC	AGTTATTGAA	750
	GAACGTGGAG	GCGGACGTCA	ACGTATTGTT	GTCAGTAAA	TTCCTTTCCA	800
	AGTGAATAAG	GCTCGTATGA	TTGAAAAAAT	TGCAGAGCTC	GTTTCGTGACA	850
45	AGAAAATTGA	CGGTATCACT	GATTTACGTG	ATGAAACAAG	TTTACGTACT	900
	GGTGTGCGTG	TCGTTATTGA	TGTGCGTAAG	GATGCAAATG	CTAGTGTCAT	950
	TTTAAATAAC	TTATACAAAC	AAACACCTCT	TCAAACATCA	TTTGGTGTGA	1000
	ATATGATTGC	ACTTGTAAT	GGTAGACCGA	AGCTTATTAA	TTTAAAAGAA	1050
	GCGTTGGTAC	ATTATTTAGA	GCATCAAAAG	ACAGTTGTGA	GAAGACGTAC	1100
50	GCAATATAAC	TTACGTAAAG	CTAAAGATCG	TGCCCATATT	TTAGAAGGGT	1150
	TACGTATCGC	ACTTGACCAT	ATCGATGAAA	TTATTTCAAC	GATTTCGTGAG	1200
	TCAGATACAG	ATAAAGTTGC	AATGGAAAGC	TTGCAACAAC	GCTTCAAAC	1250
	TTCTGAAAAA	CAAGCTCAAG	CTATTTTAGA	CATGCGTTTA	AGACGTCTAA	1300

	CAGGTTTAGA	GAGAAACAAA	ATTGAAGCTG	AATATAATGA	GTTATTAAAT	1350
	TATATTAGTG	AATTAGAAGC	CATCTTAGCT	GATGAAGAAG	TGTTATTACA	1400
	GTTAGTTAGA	GATGAATTGA	CTGAAATTAG	AGATCGTTTC	GGTGATGAGC	1450
	GTCGTACAGA	AATTCAATTA	GGTGGATTTG	AAGACTTAGA	GGACGAAGAC	1500
5	TTAATTCCAG	AAGAACAAAT	AGTAATTACT	TTGAGCCATA	ATAACTACAT	1550
	TAAACGTTTG	CCGGTATCTA	CATATCGTGC	TCAAACCCGT	GGTGGTCGTG	1600
	GTGTTCAAGG	TATGAATACA	TTGGAAGAAG	ATTTTGTTCAG	TCAATTGGTA	1650
	ACTTTAAGTA	CACATGACCA	TGTATTGTTC	TTTACTAACA	AAGGTCGTGT	1700
	ATACAAACTA	AAAGGTTATG	AAGTGCCTGA	GTTATCAAGA	CAGTCTAAAG	1750
10	GTATTCCTGT	AGTGAATGCT	ATTGAACCTG	GAAATGATGA	AGTCATTAGT	1800
	ACAATGATTG	CTGTTAAAGA	CCTTGAAAGT	GAAGACAAC	TCTTAGTGTT	1850
	TGCAACTAAA	CGTGGTGTTG	TTAAACGTTT	AGCATTAAAGT	AACTTCTCAA	1900
	GAATAAATAG	AAATGGTAAG	ATTGCGATTT	CGTTCAGAGA	AGATGATGAG	1950
	TTAATTGCAG	TTCGTTTAAC	AAGTGGTCAA	GAAGATATCT	TGATTGGTAC	2000
15	ATCACATGCA	TCATTAATTC	GATTCCCTGA	ATCAACATTA	CGTCCTTTAG	2050
	GCCGTACAGC	AACGGGTGTG	AAAGGTATTA	CACTTCGTGA	AGGTGACGAA	2100
	GTTGTAGGGC	TTGATGTAGC	TCATGCAAAC	AGTGTGATG	AAGTATTAGT	2150
	AGTTACTGAA	AATGGTTATG	GTAAACGTAC	GCCAGTTAAT	GACTATCGTT	2200
	TATCAAATCG	TGGTGGTAAA	GGTATTAAAA	CAGCTACGAT	TACTGAGCGT	2250
20	AATGGTAATG	TTGTATGTAT	CACTACAGTA	ACTGGTGAAG	AAGATTTAAT	2300
	GATTGTTACT	AATGCCGGTG	TCATTATTCG	ACTAGATGTT	GCAGATATTT	2350
	CTCAAAATGG	TCGTGCAGCA	CAAGGTGTTC	GCTTAATTCG	CTTAGGCGAT	2400
	GATCAATTTG	TTTCAACGGT	TGCTAAAGTA	AAAGAGGATG	CAGATGAAGT	2450
	AAATGAAGAT	GAACAATCTA	CTGTATCTGA	AGATGGTACT	GAACAACAAC	2500
25	GTGAAGCGGT	TGTAAATGAT	GAAACACCAG	GAAATGCAAT	TCATACTGAA	2550
	GTGATTGATT	CAGAAGAAAA	TGATGAAGAT	GGACGTATTG	AAGTAAGACA	2600
	AGATTTTCATG	GATCGTGTTG	AAGAAGATAT	ACAACAATCA	TCAGATGAAG	2650
	ATGAAGAATA	A				2711

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2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2628 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: K12
 45 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

	ATGAGCGACC	TTGCGAGAGA	AATTACACCG	GTCAACATTG	AGGAAGAGCT	50
50	GAAGAGCTCC	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	100
	TGCCAGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	150
	GCCATGAACG	TACTAGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCTGC	200
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCATCCCCAT	GGTGACTCGG	250

	CGGTCTATGA	CACGATCGTC	CGCATGGCGC	AGCCATTCTC	GCTGCGTTAT	300
	ATGCTGGTAG	ACGGTCAGGG	TAACTTCGGT	TCTATCGACG	GCGACTCTGC	350
	GGCGGCAATG	CGTTATACGG	AAATCCGTCT	GGCGAAAATT	GCCCATGAAC	400
	TGATGGCCGA	TCTCGAAAAA	GAGACGGTCG	ATTTTCGTTGA	TAACATATGAC	450
5	GGCACGGAAA	AAATTCCGGA	CGTCATGCCA	ACCAAAATTC	CTAACCTGCT	500
	GGTGAACGGT	TCTTCCGGTA	TCGCCGTAGG	TATGGCAACC	AACATCCCGC	550
	CGCACAACCT	GACGGAAGTC	ATCAACGGTT	GTCTGGCGTA	TATTGATGAT	600
	GAAGACATCA	GCATTGAAGG	GCTGATGGAA	CACATCCCGG	AGCCGGACTT	650
	CCCGACGGCG	GCAATCATTA	ACGGTCGTCT	CGGTATTGAA	GAAGCTTACC	700
10	GTACCGGTCG	CGGCAAGGTG	TATATCCGCG	CTCGCGCAGA	AGTGGAAGTT	750
	GACGCCAAAA	CCGGTCGTGA	AACCATTATC	GTCCACGAAA	TTCCGTATCA	800
	GGTAAACAAA	GCGCGCCTGA	TCGAGAAGAT	TGCGGAACTG	GTAAAAGAAA	850
	AACGCGTGGA	AGGCATCAGC	GCGCTGCGTG	ACGAGTCTGA	CAAAGACGGT	900
	ATGCGCATCG	TGATTGAAGT	GAAACGCGAT	GCGGTCGGTG	AAGTTGTGCT	950
15	CAACAACCTC	TACTCCCAGA	CCCAGTTGCA	GGTTTCTTTC	GGTATCAACA	1000
	TGGTGGCATT	GCACCATGGT	CAGCCGAAGA	TCATGAACCT	GAAAGACATC	1050
	ATCGCGGCGT	TTGTTTCGTCA	CCGCCGTGAA	GTGGTGACCC	GTCGTACTAT	1100
	TTTCGAACTG	CGTAAAGCTC	GCGATCGTGC	TCATATCCTT	GAAGCATTAG	1150
	CCGTGGCGCT	GGCGAACATC	GACCCGATCA	TCGAACTGAT	CCGTCATGCG	1200
20	CCGACGCCTG	CAGAAGCGAA	AACTGCGCTG	GTTGCTAATC	CGTGGCAGCT	1250
	GGGCAACGTT	GCCGCGATGC	TCGAACGTGC	TGGCGACGAT	GCTGCGCGTC	1300
	CGGAATGGCT	GGAGCCAGAG	TTCGGCGTGC	GTGATGGTCT	GTACTACCTG	1350
	ACCGAACAGC	AAGCTCAGGC	GATTCTGGAT	CTGCGTTTGC	AGAACTGAC	1400
	CGGTCTTGAG	CACGAAAAAC	TGCTCGACGA	ATACAAAGAG	CTGCTGGATC	1450
25	AGATCGCGGA	ACTGTTGCGT	ATTCTTGGA	GCGCCGATCG	TCTGATGGAA	1500
	GTGATCCGTG	AAGAGCTGGA	GCTGGTTCGT	GAACAGTTCG	GTGACAAACG	1550
	TCGTAATGAA	ATCACCGCCA	ACAGCGCAGA	CATCAACCTG	GAAGATCTGA	1600
	TCACCCAGGA	AGATGTGGTC	GTGACGCTCT	CTCACCAGGG	CTACGTTAAG	1650
	TATCAGCCGC	TTTCTGAATA	CGAAGCGCAG	CGTCGTGGCG	GGAAAGGTAA	1700
30	ATCTGCCGCA	CGTATTAAAG	AAGAAGACTT	TATCGACCGA	CTGCTGGTGG	1750
	CGAACACTCA	CGACCATATT	CTGTGCTTCT	CCAGCCGTGG	TCGCGTCTAT	1800
	TCGATGAAAG	TTTATCAGTT	GCCGGAAGCC	ACTCGTGGCG	CGCGCGGTCT	1850
	TCCGATCGTC	AACCTGCTGC	CGCTGGAGCA	GGACGAACGT	ATCACTGCGA	1900
	TCCTGCCAGT	GACCGAGTTT	GAAGAAGGCG	TGAAAGTCTT	CATGGCGACC	1950
35	GCTAACGGTA	CCGTGAAGAA	AACTGTCCTC	ACCGAGTTCA	ACCGTCTGCG	2000
	TACCGCCGGT	AAAGTGGCGA	TCAAACCTGGT	TGACGGCGAT	GAGCTGATCG	2050
	GCGTTGACCT	GACCAGCGGC	GAAGACGAAG	TAATGCTGTT	CTCCGCTGAA	2100
	GGTAAAGTGG	TGCGCTTTAA	AGAGTCTTCT	GTCCGTGCGA	TGGGCTGCAA	2150
	CACCACCGGT	GTTTCGCGGT	TTCGCTTAGG	TGAAGGCGAT	AAAGTCGTCT	2200
40	CTCTGATCGT	GCCTCGTGCG	GATGGCGCAA	TCCTCACCGC	AACGCAAAAC	2250
	GGTTACGGTA	AACGTACCGC	AGTGGCGGAA	TACCCAACCA	AGTCGCGTGC	2300
	GACGAAAGGG	GTTATCTCCA	TCAAGGTTAC	CGAACGTAAC	GGTTTAGTTG	2350
	TTGGCGCGGT	ACAGGTAGAT	GACTGCGACC	AGATCATGAT	GATCACCGAT	2400
	GCCGGTACGC	TGGTACGTAC	TCGCGTTTCG	GAAATCAGCA	TCGTGGGCCG	2450
45	TAACACCCAG	GGCGTGATCC	TCATCCGTAC	TGCGGAAGAT	GAAAACGTAG	2500
	TGGGTCTGCA	ACGTGTTGCT	GAACCGGTTG	ACGAGGAAGA	TCTGGATACC	2550
	ATCGACGGCA	GTGCCGCGGA	AGGGGACGAT	GAAATCGCTC	CGGAAGTGGA	2600
	CGTTGACGAC	GAGCCAGAAG	AAGAATAA			2628

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2) INFORMATION FOR SEQ ID NO: 1301

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301

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GTIMGIAWIM GICCIGSIAT GTA

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15 2) INFORMATION FOR SEQ ID NO: 1302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302

TAIADIGGIG GIKKIGCIAT RTA

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2) INFORMATION FOR SEQ ID NO: 1303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303

GGIGAIGAID YIMGIGARGG

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2) INFORMATION FOR SEQ ID NO: 1304

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

CIARYTTIKY ITTIGTYTG

19

2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

ATGGTGACTG CATTGTCAGA TG

22

2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

GTCTACGGTT TTCTACAACG TC

22

2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1923 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

5	ATGGTGACTG	CATTGTCAGA	TGTAAACAAC	ACGGATAATT	ATGGTGCTGG	50
	GCAAATACAA	GTATTAGAAG	GTTTAGAAGC	AGTACGTAAA	AGACCAGGTA	100
	TGTATATAGG	ATCGACTCAG	AGAGAGTTGC	ACATTAGTGT	GGAAATTGTC	150
	GATAATAGTA	TCGATGAAGC	ATTAGCTGGT	TATGCAAATA	AAATTGAAGT	200
	TGTTATTGAA	AAAGATAACT	GGATTAAAGT	AACGGATAAC	GGACGTGGTA	250
10	TCCCAGTTGA	TATTCAGAA	AAAATGGGAC	GTCCAGCTGT	CGAAGTTATT	300
	TTAACTGTTT	TACATGCTGG	TGGTAAATTC	GGCGGTGGCG	GATACAAAGT	350
	ATCTGGTGGT	TTACATGGTG	TTGGTTCATC	AGTTGTAAAC	GCATTGTCAC	400
	AAGACTTAGA	AGTATATGTA	CACAGAAATG	AGACTATATA	TCATCAAGCA	450
	TATAAAAAAG	GTGTACCTCA	ATTTGACTTA	AAAGAAGTTG	GCACAACTGA	500
15	TAAGACAGGT	ACTGTCATTC	GTTTTAAAGC	AGATGGAGAA	ATCTTCACAG	550
	AGACAACTGT	ATACAACTAT	GAAACATTAC	AGCAGCGTAT	TAGAGAGCTT	600
	GCTTTCCTTA	ACAAAGGAAT	TCAAATCACA	TTAAGAGATG	AACGTGATGA	650
	AGAAAACGTT	AGAGAAGACT	CCTATCACTA	TGAGGGCGGT	ATTAAATCGT	700
	ACGTTGAGTT	ATTGAACGAA	AATAAAGAAC	CTATTCATGA	TGAGCCAATT	750
20	TATATTCATC	AATCTAAAGA	TGATATTGAA	GTAGAAATTG	CGATTCAATA	800
	TAACCTCAGG	TATGCCACAA	ATCTTTTAAC	TTACGCAAAT	AACATTCATA	850
	CGTACGAAGG	TGGTACGCAT	GAAGACGGAT	TCAAACGTGC	ATTAACGCGT	900
	GTCTTAAATA	GTTATGGTTT	AAGTAGCAGA	TATGAAGAAG	AAAAGATAGC	950
	TTCTGGTGAA	GATACACGAG	AAGGTATGAC	AGCAATTATA	TCTATCAAAC	1000
25	ATGGTGATCC	TCAATTCGAA	GGTCAAACGA	AGACAAAATT	AGGTAATTCT	1050
	GAAGTGCGTC	AAGTTGTAGA	TAAATTATTC	TCAGAGCACT	TTGAACGATT	1100
	TTTATATGAA	AATCCACAAG	TCGCACGTAC	AGTGGTTGAA	AAAGGTATTA	1150
	TGGCGGCACG	TGCACGTGTT	GCTGCGAAAA	AAGCGCGTGA	AGTAACACGT	1200
	CGTAAATCAG	CGTTAGATGT	AGCAAGTCTT	CCAGGTAAAT	TAGCCGATTG	1250
30	CTCTAGTCAA	AGTCCTGAAG	AATGTGAGAT	TTTCTTAGTC	GAAGGGGACT	1300
	CTGCCGGAGG	GTCTACAAAA	TCTGGTCGTG	ACTCTAGAAC	GCAGGCGATT	1350
	TTACCATTAC	GAGGTAAGAT	ATTAAATGTT	GAAAAAGCAC	GATTAGATAG	1400
	AATTTTGAAT	AACAATGAAA	TTCGTCAAAT	GATCACAGCA	TTTGGTACAG	1450
	GAATCGGTGG	CGACTTTGAT	CTAGCGAAAG	CAAGATATCA	CAAATCGTC	1500
35	ATTATGACTG	ATGCCGATGT	GGATGGAGCG	CATATTAGAA	CATTGTTATT	1550
	AATATTCTTC	TATCGATTTA	TGAGACCGTT	AATTGAAGCA	GGCTATGTGT	1600
	ATATTGCACA	GCCACCGTTG	TATAAACTGA	CACAAGGTAA	ACAAAAGTAT	1650
	TATGTATACA	ATGATAGGGA	ACTTGATAAA	CTTAAATCTG	AATTGAATCC	1700
	AACACCAAAA	TGGTCTATTG	CGCTATACAA	AGGTCTTGGA	GAAATGAATG	1750
40	CAGATCAATT	ATGGGAAACA	ACAATGAACC	CTGAGCACCG	CGCTCTTTTA	1800
	CAAGTAA AAC	TTGAAGATGC	GATTGAAGCG	GACCAAACAT	TTGAAATGTT	1850
	AATGGGTGAC	GTTGTAGAAA	ACCGTAGACA	ATTTATAGAA	GATAATGCAG	1900
	TTTATGCAAA	CTTAGACTTC	TAA			1923

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2) INFORMATION FOR SEQ ID NO: 1308

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

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ATGTAYGTIA TIATGGAYMG IGC

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10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATATYTTTTRT TICCYTTICC YTT

23

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2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATATITSIA TIACYTCRTC

20

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2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

GARATGAARA TIMGIGGIGA RCA

23

5 2) INFORMATION FOR SEQ ID NO: 1312

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

AARTAYATIA TICARGARMG IGC

23

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2) INFORMATION FOR SEQ ID NO: 1313

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

AMIAYICKRT GIGGITTITT YTT

23

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2) INFORMATION FOR SEQ ID NO: 1314

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

TAIGAITYYA CIGAISMICA RGC

23

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2) INFORMATION FOR SEQ ID NO: 1315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315

ACIATIGCIT CIGCYTGIKS YTC

2) INFORMATION FOR SEQ ID NO: 1316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316

GTGAGTGAAA TAATTCAAGA TT

2) INFORMATION FOR SEQ ID NO: 1317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317

CACCAAAATC ATCTGTATCT AC

2) INFORMATION FOR SEQ ID NO: 1318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

10

2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCGTCIA CCATCGGYAG YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2259 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Escherichia coli*
(B) STRAIN: K-12 MG1655
(C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

45	ATGAGCGATA TGGCAGAGCG CCTTGCGCTA CATGAATTTA CGGAAAACGC	50
	CTACTTAAAC TACTCCATGT ACGTGATCAT GGACCGTGCG TTGCCGTTTA	100
	TTGGTGATGG TCTGAAACCT GTTCAGCGCC GCATTGTGTA TGCGATGTCT	150
	GAACTGGGCC TGAATGCCAG CGCCAAATTT AAAAAATCGG CCCGTACCGT	200
	CGGTGACGTA CTGGGTAAAT ACCATCCGCA CGGCGATAGC GCCTGTTATG	250
	AAGCGATGGT CCTGATGGCG CAACCGTTCT CTTACCGTTA TCCGCTGGTT	300
50	GATGGTCAGG GGAAGTGGGG CGCGCCGGAC GATCCGAAAT CGTTCGCGGC	350
	AATGCGTTAC ACCGAATCCC GGTTGTCGAA ATATTCCGAG CTGCTATTGA	400
	GCGAGCTGGG GCAGGGGACG GCTGACTGGG TGCCAAACTT CGACGGCACT	450
	TTGCAGGAGC CGAAAATGCT ACCTGCCCGT CTGCCAAACA TTTTGCTTAA	500

	CGGCACCACC	GGTATTGCCG	TCGGCATGGC	GACCGATATT	CCACCGCATA	550
	ACCTGCGTGA	AGTGGCTCAG	GCGGCAATCG	CATTAATCGA	CCAGCCGAAA	600
	ACCACGCTCG	ATCAGCTGCT	GGATATCGTG	CAGGGGCCGG	ATTATCCGAC	650
	TGAAGCGGAA	ATTATCACTT	CGCGCGCCGA	GATCCGTAAA	ATCTACGAGA	700
5	ACGGACGTGG	TTCAGTGCGT	ATGCGCGCGG	TGTGGAAGAA	AGAAGATGGC	750
	GCGGTGGTTA	TCAGCGCATT	GCCGCATCAG	GTTTCAGGTG	CGCGCGTACT	800
	GGAGCAAATT	GCTGCGCAAA	TGCGCAACAA	AAAGCTGCCG	ATGGTTGACG	850
	ATCTGCGCGA	TGAATCTGAC	CACGAGAACC	CGACCCGCCT	GGTGATTGTG	900
	CCGCGTTCCA	ACCGCGTGGA	TATGGATCAG	GTGATGAACC	ACCTCTTCGC	950
10	TACCACCGAT	CTGGAAAAGA	GCTATCGTAT	TAACCTTAAT	ATGATCGGTC	1000
	TGGATGGTCG	TCCGGCGGTG	AAAAACCTGC	TGGAAATCCT	CTCCGAATGG	1050
	CTGGTGTTCC	GCCGCGATAC	CGTGCGCCGC	CGACTGAACT	ATCGTCTGGA	1100
	GAAAGTCCTC	AAGCGCCTGC	ATATCCTCGA	AGGTTTGCTG	GTGGCGTTTC	1150
	TCAATATCGA	CGAAGTGATT	GAGATCATTC	GTAATGAAGA	TGAACCGAAA	1200
15	CCGGCGCTGA	TGTCGCGGTT	TGGCCTTACG	GAAACCCAGG	CGGAAGCGAT	1250
	CCTCGAACTG	AAACTGCGTC	ATCTTGCCAA	ACTGGAAGAG	ATGAAGATTC	1300
	GCGGTGAGCA	GAGTGAAGTG	GAAAAAGAGC	GCGACCAGTT	GCAGGGCATT	1350
	TTGGCTTCCG	AGCGTAAAT	GAATAACCTG	CTGAAGAAAG	AACTGCAGGC	1400
	AGACGCGCAA	GCCTACGGTG	ACGATCGTCG	TTCCCGTTG	CAGGAACGCG	1450
20	AAGAAGCGAA	AGCGATGAGC	GAGCACGACA	TGCTGCCGTC	TGAACCTGTC	1500
	ACCATTTGTC	TGTCGCAGAT	GGGCTGGGTA	CGCAGCGCTA	AAGGCCATGA	1550
	TATCGACGCG	CCGGGCCTGA	ATTATAAAGC	GGGTGATAGC	TTCAAAGCGG	1600
	CGGTGAAAGG	TAAGAGCAAC	CAACCGGTAG	TGTTTGTTGA	TTCCACCGGT	1650
	CGTAGCTATG	CCATTGACCC	GATTACGCTG	CCGTCGGCGC	GTGGTCAGGG	1700
25	CGAGCCGCTC	ACCGGCAAAT	TAACGTTGCC	GCCTGGGGCG	ACCGTTGACC	1750
	ATATGCTGAT	GGAAAGCGAC	GATCAGAAAC	TGCTGATGGC	TTCCGATGCG	1800
	GGTTACGGTT	TCGTCTGCAC	CTTTAACGAT	CTGGTGGCGC	GTAACCGTGC	1850
	AGGTAAGGCT	TTGATCACCT	TACCGGAAAA	TGCCCATGTT	ATGCCGCCGG	1900
	TGGTGATTGA	AGATGCTTCC	GATATGCTGC	TGGCAATCAC	TCAGGCAGGC	1950
30	CGTATGTTGA	TGTTCCCGGT	AAGTGATCTG	CCGCAGCTGT	CGAAGGGCAA	2000
	AGGCAACAAG	ATTATCAACA	TTCCATCGGC	AGAAGCCGCG	CGTGGAGAAG	2050
	ATGGTCTGGC	GCAATTGTAC	GTTCTGCCGC	CGCAAAGCAC	GCTGACCATT	2100
	CATGTTGGGA	AACGCAAAAT	TAACTGCGC	CCGGAAGAGT	TACAGAAAGT	2150
	CACTGGCGAA	CGTGGACGCC	GCGGTACGTT	GATGCGCGGT	TTGCAGCGTA	2200
35	TCGATCGTGT	TGAGATCGAC	TCTCCTCGCC	GTGCCAGCAG	CGGTGATAGC	2250
	GAAGAGTAA					2259

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2403 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: KMP9
 (C) ACCESSION NUMBER: D67074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

	GTGAGTGAAA	TAATTC AAGA	TTTATCACTT	GAAGATGTTT	TAGGTGATCG	50
5	CTTTGGAAGA	TATAGTAAAT	ATATTATTCA	AGAGCGTGCA	TTGCCAGATG	100
	TTCGTGATGG	TTTAAAACCA	GTACAACGTC	GTATTTTATA	TGCAATGTAT	150
	TCAAGTG GTA	ATACACACGA	TAAAAATTTT	CGTAAAAGTG	CGAAAAACAGT	200
	CGGTGATGTT	ATTGGTCAAT	ATCATCCACA	TGGAGACTTC	TCAGTGTACA	250
	AAGCAATGGT	CCGTTTAAGT	CAAGACTGGA	AGTTACGACA	TGTCTTAATA	300
10	GAAATGCATG	GTAATAATGG	TAGTATCGAT	AATGATCCGC	CAGCGGCAAT	350
	GCGTTACACT	GAAGCTAAGT	TAAGCTTACT	AGCTGAAGAG	TTATTACGTG	400
	ATATTAATAA	AGAGACAGTT	TCTTTCATTTC	CAAACCTATGA	TGATACGACA	450
	CTCGAACC AA	TGGTATTGCC	ATCAAGATTT	CCTAACTTAC	TAGTGAATGG	500
	TTCTACAGGT	ATATCTGCAG	GTTACGCGAC	AGATATACCA	CCACATAATT	550
15	TAGCTGAAGT	GATTCAAGCA	ACACTTAAAT	ATATTGATAA	TCCGGATATT	600
	ACAGTCAATC	AATTAATGAA	ATATATTAAA	GGTCCTGATT	TTCCAAC TGG	650
	TGGTATTATT	CAAGGTATTG	ATGGTATTAA	AAAAGCTTAT	GAATCAGGTA	700
	AAGGTAGAAT	TATAGTTCGT	TCTAAAGTTG	AAGAAGAAAC	TTTACGCAAT	750
	GGACGTAAAC	AGTTAATTAT	TACTGAAATT	CCATATGAAG	TGAACAAAAG	800
20	TAGCTTAGTA	AAACGTATCG	ATGAATTACG	TGCTGACAAA	AAAGTCGATG	850
	GTATCGTTGA	AGTACGTGAT	GAAACTGATA	GAACTGGTTT	ACGAATAGCA	900
	ATTGAATTGA	AAAAAGATGT	GAACAGTGAA	TCAATCAAAA	ATTATCTTTA	950
	TAAAAACTCT	GATTTACAGA	TTTCATATAA	TTTCAACATG	GTCGCTATTA	1000
	GTGATGGTCG	TCCAAAATTG	ATGGGTATTC	GTCAAATTAT	AGATAGTTAT	1050
25	TTGAATCATC	AAATTGAGGT	TGTTGCAAAT	AGAACGAAGT	TTGAATTAGA	1100
	TAATGCTGAA	AAACGTATGC	ATATCGTTGA	AGGTTTGATT	AAAGCGTTGT	1150
	CAATTTTAGA	TAAAGTAATT	GAATTGATTC	GTAGCTCTAA	AAACAAGCGT	1200
	GACGCTAAAG	AAAACCTTAT	CGAAGTATTC	GAGTTCACAG	AAGAACAGGC	1250
	TGAAGCAATT	GTAATGTTAC	AGTTATATCG	TTTAACAAAC	ACTGACATAG	1300
30	TTGCGCTTGA	AGGTGAACAT	AAAGA ACTTG	AAGCATTAAT	CAAACAATTA	1350
	CGTCATATTC	TTGATAACCA	TGATGCATTA	TTGAATGTCA	TAAAAGAAGA	1400
	ATTGAATGAA	ATTAAAAAGA	AATTCAAATC	TGAACGACTG	TCTTTAATTG	1450
	AAGCAGAAAT	TGAAGAAATT	AAAATTGACA	AAGAAGTTAT	GGTGCCTAGT	1500
	GAAGAAGTTA	TTTTAAGTAT	GACACGTCAT	GGATATATTA	AACGTACTTC	1550
35	TATTCG TAGC	TTTAATGCTA	GCGGTGTTGA	GGATATTGGT	TTAAAAGATG	1600
	GTGACAGTTT	ACTTAAACAT	CAAGAAGTAA	ATACGCAAGA	TACCGTACTA	1650
	GTATTTACAA	ATAAAGGTCG	TTATCTATTT	ATACCGGTTT	ATAAATTAGC	1700
	AGATATTCGT	TGGAAAGAAT	TGGGGCAACA	TGTATCACAA	ATAGTTCCTA	1750
	TCGAAGAAGA	TGAAGTG GTT	ATTAATGTCT	TTAATGAAAA	GGACTTTAAT	1800
40	ACAGATGCAT	TTTATGTTTT	TGCGACTCAA	AATGGCATGA	TTAAGAAAAG	1850
	TACAGTG CCT	CTATTTAAAA	CAACGCGTTT	TAATAAACCT	TTAATTGCTA	1900
	CTAAAGTTAA	AGAAAATGAT	GATTTGATTA	GTGTTATGCG	CTTTGAAAAA	1950
	GATCAATTAA	TTACCGTCAT	TACTAATAAA	GGTATGTCAT	TAACGTATAA	2000
	TACAAGTGAA	CTATCAGATA	CCGGATTAAAG	GGCAGCTGGT	GTTAAATCAA	2050
45	TAAATCTTAA	AGCTGAAGAT	TTCGTTGTTA	TGACAGAAGG	TGTTTCTGAA	2100
	AATGATACTA	TATTGATGGC	CACACAACGC	GGCTCGTTAA	AACGTATTAG	2150
	TTTTTAAATC	TTACAAGTTG	CTAAAAGAGC	ACAACGTGGA	ATAACTTTAT	2200
	TAAAAGAATT	AAAGAAAAAT	CCACATCGTA	TTGTAGCTGC	ACATGTAGTG	2250
	ACAGGTGAAC	ATAGTCAATA	TACATTATAT	TCAAAATCAA	ATGAAGAACA	2300
50	TGGTTTAATT	AATGATATTC	ATAAATCTGA	ACAATATACA	AATGGCTCAT	2350
	TCATTGTAGA	TACAGATGAT	TTTGGTGAAG	TAATAGACAT	GTATATTAGC	2400
	TAA					2403

2) INFORMATION FOR SEQ ID NO: 1322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIAAYI SIGTIGAYGA RG

22

2) INFORMATION FOR SEQ ID NO: 1323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

2) INFORMATION FOR SEQ ID NO: 1324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

CCICCGICIS WRTCICCYTC

20

2) INFORMATION FOR SEQ ID NO: 1325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

RTTCATYTCI CCIARICCYT T

21

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

TGATTCAATA CAGGTTTTAG AG

22

25

2) INFORMATION FOR SEQ ID NO: 1327

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

40 CTAGATTTC TCCTCATCAA AT

22

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: RN4220
 (C) ACCESSION NUMBER: D67075

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

	ATGAATAAAC	AAAATAATTA	TTCAGATGAT	TCAATACAGG	TTT TAGAGGG	50
	GTTAGAAGCA	GTTTCGTAAA	GACCTGGTAT	GTATATTGGA	TCAACTGATA	100
10	AACGGGGATT	ACATCATCTA	GTATATGAAA	TTGTCGATAA	CTCCGTCGAT	150
	GAAGTATTGA	ATGGTTACGG	TAACGAAATA	GATGTAACAA	TTAATAAAGA	200
	TGGTAGTATT	TCTATAGAAG	ATAATGGACG	TGGTATGCCA	ACAGGTATAC	250
	ATAAATCAGG	TAAACCGACA	GTCGAAGTTA	TCTTTACTGT	TTTACATGCA	300
	GGAGGTAAAT	TTGGACAAGG	CGGCTATAAA	ACTTCAGGTG	GTCTTCACGG	350
15	TGTTGGTGCT	TCAGTTGTAA	ATGCATTGAG	TGAATGGCTT	GAAGTTGAAA	400
	TCCATCGAGA	TGGTAATATA	TATCATCAAA	GTTTTAAAAA	CGGTGGTTCG	450
	CCATCTTCTG	GTTTAGTGAA	AAAAGGTAAA	ACTAAGAAAA	CAGGTACCAA	500
	AGTAACATTT	AAACCTGATG	ACACAATTTT	TAAAGCATCT	ACATCATTTA	550
	ATTTTGATGT	TTTAAGTGAA	CGACTACAAG	AGTCTGCGTT	CTTATTGAAA	600
20	AATTTAAAAA	TAACGCTTAA	TGATTTACGC	AGTGGTAAAG	AGCGTCAAGA	650
	GCATTACCAT	TATGAAGAAG	GAATCAAAGA	GTTTGTTAGT	TATGTCAATG	700
	AAGGAAAAGA	AGTTTTGCAT	GACGTGGCTA	CATTTTCAGG	TGAAGCAAAT	750
	GGTATAGAGG	TAGACGTAGC	TTTCCAATAT	AATGATCAAT	ATTCAGAAAG	800
	TATTTTAAGT	TTTGTAATA	ATGTACGTAC	TAAAGATGGT	GGTACACATG	850
25	AAGTTGGTTT	TAAAACAGCA	ATGACACGTG	TATTTAATGA	TTATGCACGT	900
	CGTATTAATG	AACTTAAAC	AAAAGATAAA	AACTTAGATG	GTAATGATAT	950
	TCGTGAAGGT	TTAACAGCTG	TTGTGTCTGT	TCGTATTCCA	GAAGAATTAT	1000
	TGCAATTTGA	AGGACAAACG	AAATCTAAAT	TGGGTACTTC	TGAAGCTAGA	1050
	AGTGCTGTTG	ATTCAGTTGT	TGCAGACAAA	TTGCCATTCT	ATTTAGAAGA	1100
30	AAAAGGACAA	TTGTCTAAAT	CACTTG TGAA	AAAAGCGATT	AAAGCACAAAC	1150
	AAGCAAGGGA	AGCTGCACGT	AAAGCTCGTG	AAGATGCTCG	TTCAGGTAAG	1200
	AAAAACAAGC	GTAAAGACAC	TTTGCTATCT	GGTAAATTAA	CACCTGCACA	1250
	AAGTAAAAAC	ACTGAAAAAA	ATGAATTGTA	TTTAGTCGAA	GGTGATTCTG	1300
	CGGGAGGTTT	AGCAAAACTT	GGACGAGACC	GCAAATTCCA	AGCGATATTA	1350
35	CCATTACGTG	GTAAGGTAAT	TAATACAGAG	AAAGCACGTC	TAGAAGATAT	1400
	TTTTAAAAAT	GAAGAAATTA	ATACAATTAT	CCACACAATC	GGGGCAGGCG	1450
	TTGGTACTGA	CTTTAAAATT	GAAGATAGTA	ATTATAATCG	TGTAATTATT	1500
	ATGACTGATG	CTGATACTGA	TGGTGCGCAT	ATTCAAGTGC	TATTGTTAAC	1550
	ATTCTTCTTC	AAATATATGA	AACCGCTTGT	TCAAGCAGGT	CGTGTATTTA	1600
40	TTGCTTTACC	TCCACTTTAT	AAATTGGAAA	AAGGTAAAGG	CAAAACAAAG	1650
	CGAGTTGAAT	ACGCTTGGAC	AGACGAAGAG	CTTAATAAAT	TGCAAAAAGA	1700
	ACTTGGTAAA	GGCTTCACGT	TACAACGTTA	CAAAGGTTTG	GGTGAAATGA	1750
	ACCTTGAGCA	ATTATGGGAA	ACGACGATGA	ACCCAGAAAC	ACGAAC TT TA	1800
	ATTCGTGTAC	AAGTTGAAGA	TGAAGTGCGT	TCATCTAAAC	GTGTAACAAC	1850
45	ATTAATGGGT	GACAAAGTAC	AACCTAGACG	TGAATGGATT	GAAAAGCATG	1900
	TTGAGTTTGG	TATGCAAGAG	GACCAAAGTA	TTTTAGATAA	TTCTGAAGTA	1950
	CAAGTGCTTG	AAAATGATCA	ATTTGATGAG	GAGGAAATCT	AG	1992

50

2) INFORMATION FOR SEQ ID NO: 1329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

10 TGTAGAGCGC GGTATCATCA AAGTA

25

2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

25

AGATTCGAAC TTGGTGTGCG GG

22

30 2) INFORMATION FOR SEQ ID NO: 1331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

40

GCCCTTGAGG TACAGAATGG TAATGAAGTT

30

45

2) INFORMATION FOR SEQ ID NO: 1332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA

20

10 2) INFORMATION FOR SEQ ID NO: 1333

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

CATCTATTTA TAAAGCAATG GTA

23

40

2) INFORMATION FOR SEQ ID NO: 1335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

CTATTTATGG AGCAATGGT

19

2) INFORMATION FOR SEQ ID NO: 1336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

2) INFORMATION FOR SEQ ID NO: 1337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

2) INFORMATION FOR SEQ ID NO: 1338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

GTGTACGGAG CAATG

15

2) INFORMATION FOR SEQ ID NO: 1339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TCGGT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

GATAACTGAA ATCCTGAGCC ATACG

25

40

2) INFORMATION FOR SEQ ID NO: 1342

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

20

29

2) INFORMATION FOR SEQ ID NO: 1344

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

2) INFORMATION FOR SEQ ID NO: 1346

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

2) INFORMATION FOR SEQ ID NO: 1347

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

2) INFORMATION FOR SEQ ID NO: 1348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Unidentified bacterium
- (C) ACCESSION NUMBER: X04555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

ATGCGCTCAC	GCAACTGGTC	CAGAACCTTG	ACCGAACGCA	GCGGTGGTAA	50
CGGCGCAGTG	GCGGTTTTCA	TGGCTTGTTA	TGACTGTTTT	TTTGTACAGT	100
CTATGCCTCG	GGCATCCAAG	CAGCAAGCGC	GTTACGCCGT	GGGTCGATGT	150
TTGATGTTAT	GGAGCAGCAA	CGATGTTACG	CAGCAGGGCA	GTCGCCCTAA	200
AACAAAGTTA	GGCCGCATGG	ACACAACGCA	GGTCACATTG	ATACACAAAA	250

	TTCTAGCTGC	GGCAGATGAG	CGAAATCTGC	CGCTCTGGAT	CGGTGGGGGC	300
	TGGGCGATCG	ATGCACGGCT	AGGGCGTGTA	ACACGCAAGC	ACGATGATAT	350
	TGATCTGACG	TTTCCCGGCG	AGAGGCGCGG	CGAGCTCGAG	GCAATAGTTG	400
	AAATGCTCGG	CGGGCGCGTC	ATGGAGGAGT	TGGACTATGG	ATTCTTAGCG	450
5	GAGATCGGGG	ATGAGTTACT	TGACTGCGAA	CCTGCTTGGT	GGGCAGACGA	500
	AGCGTATGAA	ATCGCGGAGG	CTCCGCAGGG	CTCGTGCCCA	GAGGCGGCTG	550
	AGGGCGTCAT	CGCCGGGCGG	CCAGTCCGTT	GTAACAGCTG	GGAGGCGATC	600
	ATCTGGGATT	ACTTTTACTA	TGCCGATGAA	GTACCACCAG	TGGACTGGCC	650
	TACAAAGCAC	ATAGAGTCCT	ACAGGCTCGC	ATGCACCTCA	CTCGGGGCGG	700
10	AAAAGGTTGA	GGTCTTGCGT	GCCGCTTTCA	GGTCGCGATA	TGCGGCCTAA	750

2) INFORMATION FOR SEQ ID NO: 1349

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

30 2) INFORMATION FOR SEQ ID NO: 1350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

40

TAATCAGGGC AGTTGCGACT CCTA

24

45

2) INFORMATION FOR SEQ ID NO: 1351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: Stone 130
 (C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

10	ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAAC	50
	AAAGTTAGGT GGCTCAATGA GCATCATTCG AACCGTCAAG ATCGGCCCTG	100
	ACGAAATTTT AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT	150
	GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC	200
	CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG	250
15	GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCCAA GTTCGAGCAA	300
	GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG	350
	AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG	400
	TTGAACTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CGGTGACGAT	450
	CCGGCAGTCG CTCTCTACAC AAAGCTTGA GTTCGGGAAG ACGTCATGCA	500
20	CTTCGACATT GATCCAAGAA CCGCCACCTA A	531

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG

22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG

22

2) INFORMATION FOR SEQ ID NO: 1354

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

2) INFORMATION FOR SEQ ID NO: 1355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

2) INFORMATION FOR SEQ ID NO: 1356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M97172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

ATGAACACGA	TCGAATCGAT	CACGGCGGAC	CTGCACGGAC	TGGGCGTCCG	50
GCCCCGGCGAC	CTGATCATGG	TCCATGCATC	GCTGAAAGCC	GTCGGCCCCGG	100
TCGAGGGGAGG	TGCGGCCTCG	GTGGTGTCTCG	CCCTTCGCGC	CGCGGTCGGG	150
TCCGCAGGGA	CCCTGATGGG	TTATGCCTCA	TGGGACCGCT	CGCCCTATGA	200
GGAGACGCTG	AACGGCGCGC	GGATGGACGA	AGAACTGCGC	CGCCGGTGGC	250

	CACCCTTCGA	TCTGGCCACA	TCCGGTACCT	ATCCCGGCTT	CGGCCTGCTC	300
	AACCGGTTTC	TGCTTGAGGC	GCCCGACGCA	CGGCGCAGCG	CGCATCCCGA	350
	CGCCTCCATG	GTCGCGGTCG	GCCCCCTTGC	CGCCACGCTG	ACAGAGCCGC	400
	ACCGGCTTGG	GCAGGCGCTG	GGCGAAGGCT	CGCCGCTGGA	GCGCTTCGTC	450
5	GGGCATGGCG	GAAAGGTCCT	GCTTCTGGGA	GCGCCGCTCG	ACTCCGTCAC	500
	CGTGCTGCAT	TACGCCGAGG	CCATCGCCCC	CATCCCGAAC	AAACGCCGCG	550
	TGACCTATGA	AATGCCGATG	CTCGGCCCGG	ATGGCAGGGT	CCGATGGGAG	600
	CTGGCCGAGG	ATTTGACAG	CAACGGCATT	CTCGATTGCT	TCGCGGTCGA	650
	TGGGAAGCCG	GATGCCGTCG	AGACGATCGC	CAAGGCTTAT	GTCGAACTGG	700
10	GCCGGCATCG	GGAAGGCATC	GTCGGTCGCG	CACCTCCTA	TCTGTTTGAA	750
	GCGCAGGATA	TCGTCTCGTT	CGGCGTCACC	TATCTCGAAC	AGCATTTTCG	800
	CGCGCCCTGA					810

15

2) INFORMATION FOR SEQ ID NO: 1357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

2) INFORMATION FOR SEQ ID NO: 1358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

2) INFORMATION FOR SEQ ID NO: 1359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCTGCC ACCTCACTC

19

10

2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25

2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 786 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X01385

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

	GTGCAATACG AATGGCGAAA AGCCGAGCTC ATCGGTCAGC TTCTCAACCT	50
	TGGGGTTACC CCCGGCGGTG TGCTGCTGGT CCACAGCTCC TTCCGTAGCG	100
45	TCCGGCCCCCT CGAAGATGGG CCACTTGGAC TGATCGAGGC CCTGCGTGCT	150
	GCGCTGGGTC CGGGAGGGAC GCTCGTCATG CCCTCGTGGT CAGGTCTGGA	200
	CGACGAGCCG TTCGATCCTG CCACGTCGCC CGTTACACCG GACCTTGGAG	250
	TTGTCTCTGA CACATTCTGG CGCCTGCCAA ATGTAAAGCG CAGCGCCCAT	300
	CCATTTGCCT TTGCGGCAGC GGGGCCACAG GCAGAGCAGA TCATCTCTGA	350
50	TCCATTGCCC CTGCCACCTC ACTCGCCTGC AAGCCCGGTC GCCCGTGTCC	400
	ATGAACTCGA TGGGCAGGTA CTTCTCCTCG GCGTGGGACA CGATGCCAAC	450
	ACGACGCTGC ATCTTGCCGA GTTGATGGCA AAGGTTCCCT ATGGGGTGCC	500
	GAGACACTGC ACCATTCTTC AGGATGGCAA GTTGGTACGC GTCGATTATC	550

TCGAGAATGA CCACTGCTGT GAGCGCTTTG CCTTGGCGGA CAGGTGGCTC 600
 AAGGAGAAGA GCCTTCAGAA GGAAGGTCCA GTCGGTCATG CCTTTGCTCG 650
 GTTGATCCGC TCCCGCGACA TTGTGGCGAC AGCCCTGGGT CAACTGGGCC 700
 GAGATCCGTT GATCTTCCTG CATCCGCCAG AGGGCGGGAT GCGAAGAATG 750
 5 CGATGCCGCT CGCCAGTCGA TTGGCTGAGC TCATGA 786

2) INFORMATION FOR SEQ ID NO: 1362

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

CGCCGCCATC GCCCAAAGCT GG

22

2) INFORMATION FOR SEQ ID NO: 1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

CGGCATAATG GAGCGCGGTG ACTG

24

2) INFORMATION FOR SEQ ID NO: 1364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

TTTCTCGCCC ACGCAGGAAA AATC

24

2) INFORMATION FOR SEQ ID NO: 1365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

2) INFORMATION FOR SEQ ID NO: 1366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (C) ACCESSION NUMBER: M88012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

ATGACTGATC	CCCGCAAAAA	CGGCGATTTG	CACGAACCCG	CGACGGCACC	50
CGCGACGCCC	TGGTCCAAAA	GCGAGCTGGT	CCGGCAATTG	CGCGACCTCG	100
GCGTGCGCTC	AGGCGATATG	GTGATGCCGC	ATGTGTCGTT	GCGCGCCGTC	150
GGGCCGCTGG	CGGACGGACC	GCAGACACTT	GTCGATGCGC	TGATCGAGGC	200
CGTCGGCCCC	ACCGGGAATA	TTCTCGCCTT	CGTCTCGTGG	CGCGATTTCGC	250
CCTATGAACA	GACGCTGGGT	CATGATGCGC	CGCCCGCCGC	CATCGCCCCA	300
AGCTGGCCTG	CGTTCGACCC	CGACCATGCG	CCCGCCTACC	CCGGCTTTGG	350
CGCGATCAAC	GAATTTATCC	GAACCTATCC	GGGGTGTCGG	CGCACGGCCC	400
ATCCCGACGC	ATCGATGGCG	GCGATCGGGC	CCGATGCGGC	GTGGCTGGTG	450
GCGCCGCACG	AGATGGGCGC	CGCTTATGGC	CCCCGCTCGC	CGATCGCGCG	500
TTTTCTCGCC	CACGCAGGAA	AAATCCTGTC	GATCGGCGCC	GGGCCCAGATG	550
CAGTCACCGC	GCTCCATTAT	GCCGAAGCGG	TGGCGCGGAT	CGAGGGCAAG	600
CGCCGCGTCA	CTTATTCGAT	GCCCTTACTG	CGCGAAGGCA	AGCGCGTCTG	650
GGTCACCACG	TCCGACTGGG	ATTGCAACGG	CATCCTCGAC	GAATATGCCG	700
CGCCCGACGG	CCCCGACGCG	GTCGAACGGA	TCGCCCCGCA	CTATCTCGCC	750
CGCACCAGGG	TTGCGCAAGG	CCCGGTCGGC	GGCGCGCAAT	CCCGGCTGAT	800
CGACGCGGCC	GATATCGTTT	CCTTCGGCAT	CGAATGGCTC	GAGGCGCGCC	850
ACGCCGCGCC	AGCGGCGGCA	GCGCTGAAGC	CGAAACAACG	CCGCGACTGA	900

2) INFORMATION FOR SEQ ID NO: 1367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

2) INFORMATION FOR SEQ ID NO: 1368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

2) INFORMATION FOR SEQ ID NO: 1369

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

AAACCTTTGT TTCGGTCTGC TAAT

24

2) INFORMATION FOR SEQ ID NO: 1370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 558 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter diversus*
(C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

	ATGAATTATC	AAATTGTGAA	TATTGCGGAA	TGCAGCAATT	ATCAGTTAGA	50
	AGCAGCAAAT	ATACTAACAG	AAGCGTTCAA	TGATCTTGGT	AACAATTCAT	100
30	GGCCAGATAT	GACGAGTGCA	ACAAAAGAAG	TAAAAGAATG	TATTGAGAGT	150
	CCAAACCTTT	GTTTCGGTCT	GCTAATAAAT	AACTCCTTAG	TTGGCTGGAT	200
	AGGCTTAAGG	CCAATGTACA	AGGAAACCTG	GGAATTGCAT	CCATTGGTTG	250
	TCAGACCAGA	TTATCAAAAT	AAAGGTATTG	GCAAGATCCT	GCTTAAGGAA	300
	TTAGAAAACA	GAGCTAGAGA	GCAAGGTATT	ATTGGAATCG	CTTTAGGAAC	350
35	AGATGATGAA	TACTATAGAA	CAAGTCTCTC	TTTAATAACT	ATAACAGAAG	400
	ATAATATATT	TGATTCAATA	AAAAATATTA	AAAATATTAA	TAAACATCCA	450
	TATGAGTTTT	ATCAGAAGAA	TGGTTATTAT	ATTGTTGGAA	TAATTCCAAA	500
	TGCCAATGGT	AAAAACAAAC	CAGATATTTG	GATGTGGAAA	AGTTTAATCA	550
	AAGAGTAA					558

40

2) INFORMATION FOR SEQ ID NO: 1372

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TTCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1376

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M94066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

ATGATCGTCA	TCTGCGACCA	CGACAACCTC	GACGCCTGGC	TGGCGCTGCG	50
CACCGCGCTG	TGGCCCTCCG	GCTCGCCTGA	AGATCACCGC	GCGGAAATGC	100
GCGAGATATT	GGCTTCGCCG	CACCACACCG	CGTTTATGGC	GCGGGGGCTG	150
GACGGCGCTT	TCGTTGCCTT	TGCCGAGGTC	GCGCTGCGCT	ACGATTACGT	200
CAACGGCTGC	GAATCGTCGC	CGGTGGCGTT	TTTGGAAGGA	ATTTATACCG	250
CCGAACGCGC	CCGCCGCCAG	GGCTGGGCCG	CGCGCCTGAT	CGCGCAGGTG	300
CAGGAGTGGG	CGAAGCAACA	GGGGTGCAGC	GAGCTGGCGT	CGGATACCGA	350
TATCGCCAAT	CTGGACTCCC	AGCGCCTGCA	TGCGGCGCTG	GGCTTTGCCG	400
AAACGGAGCG	AGTAGTGTTT	TACCGCAAAA	CGCTGGGCTG	A	441

2) INFORMATION FOR SEQ ID NO: 1377

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

GCCGTGGGTC GATGTTTGAT GTTA

24

2) INFORMATION FOR SEQ ID NO: 1378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

2) INFORMATION FOR SEQ ID NO: 1379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

CGCTCGATGA CGCCAACTAC CTCT

24

2) INFORMATION FOR SEQ ID NO: 1381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

	GTGGTAACGG	CGCAGTGGCG	GTTTTTCATGG	CTTCTTGTTA	TGACATGTTT	50
	TTTTGGGGTA	CAGTCTATGC	CTCGGGCATC	CAAGCAGCAA	GCGCGTTACG	100
5	CCGTGGGTCG	ATGTTTGATG	TTATGGAGCA	GCAACGATGT	TACGCAGCAG	150
	GGCAGTCGCC	CTAAAACAAA	GTTAAACATC	ATGAGGGAAG	CGGTGATCGC	200
	CGAAGTATCG	ACTCAACTAT	CAGAGGTAAGT	TGGCGTCATC	GAGCGCCATC	250
	TCGAACCGAC	GTTGCTGGCC	GTACATTTGT	ACGGCTCCGC	AGTGGATGGC	300
	GGCCTGAAGC	CACACAGTGA	TATTGATTTG	CTGGTTACGG	TGACCGTAAG	350
10	GCTTGATGAA	ACAACGCGGC	GAGCTTTGAT	CAACGACCTT	TTGGAAACTT	400
	CGGCTTCCCC	TGGAGAGAGC	GAGATTCTCC	GCGCTGTAGA	AGTCACCATT	450
	GTTGTGCACG	ACGACATCAT	TCCGTGGCGT	TATCCAGCTA	AGCGCGAACT	500
	GCAATTTGGA	GAATGGCAGC	GCAATGACAT	TCTTGAGGT	ATCTTCGAGC	550
	CAGCCACGAT	CGACATTGAT	CTGGCTATCT	TGCTGACAAA	AGCAAGAGAA	600
15	CATAGCGTTG	CCTTGGTAGG	TCCAGCGGCG	GAGGAACTCT	TTGATCCGGT	650
	TCCTGAACAG	GATCTATTTG	AGGCGCTAAA	TGAAACCTTA	ACGCTATGGA	700
	ACTCGCCGCC	CGACTGGGCT	GGCGATGAGC	GAAATGTAAGT	GCTTACGTTG	750
	TCCCGCATTT	GGTACAGCGC	AGTAACCGGC	AAAATCGCGC	CGAAGGATGT	800
	CGCTGCCGAC	TGGGCAATGG	AGCGCCTGCC	GGCCCAGTAT	CAGCCCGTCA	850
20	TACTTGAAGC	TAGACAGGCT	TATCTTGGAC	AAGAAGAAGA	TCGCTTGGCC	900
	TCGCGCGCAG	ATCAGTTGGA	AGAATTTGTC	CACTACGTGA	AAGGCGAGAT	950
	CACCAAGGTA	GTCGGCAAAT	AA			972

25

2) INFORMATION FOR SEQ ID NO: 1382

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 24 bases
30	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Single
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 23 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Single
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

5 2) INFORMATION FOR SEQ ID NO: 1384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

2) INFORMATION FOR SEQ ID NO: 1385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

2) INFORMATION FOR SEQ ID NO: 1386

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- 50 (C) ACCESSION NUMBER: V01282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50

CGAGGAAAGT GGAGAAGTAA TAGAGGTAGA TAAGCTATAC CGTAAACAAA 100
 CGTCTGGTAA CTTTGTAATA GCGTATATCG TCCAATTAAT AAGTATGTTA 150
 GATATGATAG GCGGTAAAAA GCTCAAGATT GTTAATTATA TATTAGATAA 200
 TGTACATCTA AGTAATAACA CAATGATAGC AACTGTTAGA GAAATAGCAG 250
 5 AAGGAACAAA TACAAGCACG AAAACCGTAA ATACAACGCT TAAAATCTTA 300
 GAAGAAGGAA ATATCATTA AAGAAGAAGT GGAGCATTA TGCTAAACCC 350
 AGAGCTACTC ATGAGAGGCG ATGACCAAAA ACAAAAATAC CTCTTACTCG 400
 AATTTGGGAA CTTTGAGCAA GAGGACGACC AAAAGCAAGA AAATGCTTTA 450
 TCAGAATATT ATTCTTTCAA GGAGTAG 477
 10

2) INFORMATION FOR SEQ ID NO: 1387

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387
 25 TTATGCCTCT TCCGACCATC AAGC 24

2) INFORMATION FOR SEQ ID NO: 1388

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388
 40 TACGCTCGTC ATCAAAATCA CTCG 24

2) INFORMATION FOR SEQ ID NO: 1389

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

2) INFORMATION FOR SEQ ID NO: 1390

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

40	ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC	50
	CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG	100
	GGCAATCAGG TGCACAAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA	150
	GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA	200
	TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCCGACCA	250
45	TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTTACT CACCACTGCG	300
	ATCCCCGGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG	350
	TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCTGA	400
	TTCCTGTTTG TAATTGTCCT TTTAACAGCG ATCGCGTATT TCGTCTCGCT	450
	CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA	500
50	TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA	550
	AGCTTTTGCC ATTCTCACCG GATTCAGTCG TCACTCATGG TGATTCTCTCA	600
	CTTGATAACC TTATTTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT	650
	TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA	700

ACTGCCTCGG TGAGTTTTCT CCTTCATTAC AGAAACGGCT TTTTCAAAAA 750
TATGGTATTG ATAATCCTGA TATGAATAAA TTGCAGTTTC ATTTGATGCT 800
CGATGAGTTT TTCTAA 816

5

2) INFORMATION FOR SEQ ID NO: 1392

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

20 TGGGTGGAGA GGCTATTCGG CTAT

24

2) INFORMATION FOR SEQ ID NO: 1393

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC

23

2) INFORMATION FOR SEQ ID NO: 1394

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

50

GACGTTGTCA CTGAAGCGGG AAGG

24

2) INFORMATION FOR SEQ ID NO: 1395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

2) INFORMATION FOR SEQ ID NO: 1396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: V00618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

ATGATTGAAC	AAGATGGATT	GCACGCAGGT	TCTCCGGCCG	CTTGGGTGGA	50
GAGGCTATTC	GGCTATGACT	GGGCACAACA	GACAATCGGC	TGCTCTGATG	100
CCGCCGTGTT	CCGGCTGTCA	GCGCAGGGGC	GCCCGGTTCT	TTTTGTCAAG	150
ACCGACCTGT	CCGGTGCCCT	GAATGAACTG	CAGGACGAGG	CAGCGCGGCT	200
ATCGTGGCTG	GCCACGACGG	GCGTTCCTTG	CGCAGCTGTG	CTCGACGTTG	250
TCACTGAAGC	GGGAAGGGAC	TGGCTGCTAT	TGGGCGAAGT	GCCGGGGCAG	300
GATCTCCTGT	CATCTCACCT	TGCTCCTGCC	GAGAAAGTAT	CCATCATGGC	350
TGATGCAATG	CGGCGGCTGC	ATACGCTTGA	TCCGGCTACC	TGCCCATTTCG	400
ACCACCAAGC	GAAACATCGC	ATCGAGCGAG	CACGTACTCG	GATGGAAGCC	450
GGTCTTGTCG	ATCAGGATGA	TCTGGACGAA	GAGCATCAGG	GGCTCGCGCC	500
AGCCGAACTG	TTCGCCAGGC	TCAAGGCGCG	CATGCCCGAC	GGCGAGGATC	550
TCGTCGTGAC	CCATGGCGAT	GCCTGCTTGC	CGAATATCAT	GGTGGAAAAT	600
GGCCGCTTTT	CTGGATTTCAT	CGACTGTGGC	CGGCTGGGTG	TGGCGGACCG	650
CTATCAGGAC	ATAGCGTTGG	CTACCCGTGA	TATTGCTGAA	GAGCTTGGCG	700
GCGAATGGGC	TGACCGCTTC	CTCGTGCTTT	ACGGTATCGC	CGCTCCCGAT	750
TCGCAGCGCA	TCGCCTTCTA	TCGCCTTCTT	GACGAGTTCT	TCTGA	795

2) INFORMATION FOR SEQ ID NO: 1397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397

GTGGGAGAAA ATGAAAACCT AT

2) INFORMATION FOR SEQ ID NO: 1398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398

ATGGAGTGAA AGAGCCTGAT

2) INFORMATION FOR SEQ ID NO: 1399

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399

ACCTATGATG TGGAACGGGA AAAG

2) INFORMATION FOR SEQ ID NO: 1400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

CGATGGAGTG AAAGAGCCTG ATG

23

2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

ATGGCTAAAA	TGAGAATATC	ACCGGAATTG	AAAAAACTGA	TCGAAAAATA	50
CCGCTGCGTA	AAAGATACGG	AAGGAATGTC	TCCTGCTAAG	GTATATAAGC	100
TGGTGGGAGA	AAATGAAAAC	CTATATTTAA	AAATGACGGA	CAGCCGGTAT	150
AAAGGGACCA	CCTATGATGT	GGAACGGGAA	AAGGACATGA	TGCTATGGCT	200
GGAAGGAAAG	CTGCCTGTTT	CAAAGGTCCT	GCACTTTGAA	CGGCATGATG	250
GCTGGAGCAA	TCTGCTCATG	AGTGAGGCCG	ATGGCGTCCT	TTGCTCGGAA	300
GAGTATGAAG	ATGAACAAAG	CCCTGAAAAG	ATTATCGAGC	TGTATGCGGA	350
GTGCATCAGG	CTCTTTCAC	CCATCGACAT	ATCGGATTGT	CCCTATACGA	400
ATAGCTTAGA	CAGCCGCTTA	GCCGAATTGG	ATTACTTACT	GAATAACGAT	450
CTGGCCGATG	TGGATTGCGA	AAACTGGGAA	GAAGACACTC	CATTTAAAGA	500
TCCGCGCGAG	CTGTATGATT	TTTTAAAGAC	GGAAAAGCCC	GAAGAGGAAC	550
TTGTCTTTTC	CCACGGCGAC	CTGGGAGACA	GCAACATCTT	TGTGAAAGAT	600
GGCAAAGTAA	GTGGCTTTAT	TGATCTTGGG	AGAAGCGGCA	GGGCGGACAA	650
GTGGTATGAC	ATTGCCTTCT	GCGTCCGGTC	GATCAGGGAG	GATATCGGGG	700
AAGAACAGTA	TGTCGAGCTA	TTTTTTGACT	TACTGGGGAT	CAAGCCTGAT	750
TGGGAGAAAA	TAAAATATTA	TATTTTACTG	GATGAATTGT	TTTAG	795

2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

TATTCAACAA TTTATCGGAA ACAG

24

2) INFORMATION FOR SEQ ID NO: 1403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

TCAGAGAGCC AACTCAACAT TTT

23

2) INFORMATION FOR SEQ ID NO: 1404

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

AAACAGCGTT TTAGAGCCAA ATAA

24

2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT

24

2) INFORMATION FOR SEQ ID NO: 1406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: BM2580
(C) ACCESSION NUMBER: X07753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

ATGGAATTGC	CCAATATTAT	TCAACAATTT	ATCGGAAACA	GCGTTTTAGA	50
GCCAAATAAA	ATTGGTCAGT	CGCCATCGGA	TGTTTATTCT	TTTAATCGAA	100
ATAATGAAAC	TTTTTTTCTT	AAGCGATCTA	GCACTTTATA	TACAGAGACC	150
ACATACAGTG	TCTCTCGTGA	AGCGAAAATG	TTGAGTTGGC	TCTCTGAGAA	200
ATTAAAGGTG	CCTGAACTCA	TCATGACTTT	TCAGGATGAG	CAGTTTGAAT	250
TCATGATCAC	TAAAGCGATC	AATGCAAAAC	CAATTCAGC	GCTTTTTTTA	300
ACAGACCAAG	AATTGCTTGC	TATCTATAAG	GAGGCACTCA	ATCTGTTAAA	350
TTCAATTGCT	ATTATTGATT	GTCCATTTAT	TTCAAACATT	GATCATCGGT	400
TAAAAGAGTC	AAAATTTTTT	ATTGATAACC	AACTCCTTGA	CGATATAGAT	450
CAAGATGATT	TTGACACTGA	ATTATGGGGA	GACCATAAAA	CTTACCTAAG	500
TCTATGGAAT	GAGTTAACCG	AGACTCGTGT	TGAAGAAAGA	TTGGTTTTTT	550
CTCATGGCGA	TATCACGGAT	AGTAATATTT	TTATAGATAA	ATTCAATGAA	600
ATTTATTTTT	TAGATCTTGG	TCGTGCTGGG	TTAGCAGATG	AATTTGTAGA	650
TATATCCTTT	GTTGAACGTT	GCCTAAGAGA	GGATGCATCG	GAGGAAACTG	700
CGAAAATATT	TTTAAAGCAT	TTAAAAAATG	ATAGACCTGA	CAAAGGAAT	750
TATTTTTTAA	AACTTGATGA	ATTGAATTGA			780

2) INFORMATION FOR SEQ ID NO: 1407

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

24

2) INFORMATION FOR SEQ ID NO: 1408

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408

TTGTCGTATC CCTCAAATCA CC

22

15 2) INFORMATION FOR SEQ ID NO: 1409

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409

TGGGATTACA ATGGCAATCA GCG

23

30 2) INFORMATION FOR SEQ ID NO: 1410

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410

GGGGAATAGG TCACAAGATC TGCTT

25

45 2) INFORMATION FOR SEQ ID NO: 1411

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 912 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

```

10  ATGCTTTTAT ATAAAATGTG TGACAATCAA AATTATGGGG TTACTTACAT      50
    GAAGTTTTTA TTGGCATTTT CGCTTTTAAT ACCATCCGTG GTTTTTGCAA      100
    GTAGTTCAAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT      150
    TCTCTTTCTG CTCGTATAGG TGTTTCCGTT CTTGATACTC AAAATGGAGA      200
15  ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA      250
    AAACAATAGC TTGCGCTAAA TTACTATATG ATGCTGAGCA AGGAAAAGTT      300
    AATCCCAATA GTACAGTCGA GATTAAGAAA GCAGATCTTG TGACCTATTC      350
    CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT      400
    GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAAA TATCATCCTA      450
20  AGTGCTGTAG GTGGCCCCAA AGGCGTTACT GATTTTTTAA GACAAATTGG      500
    GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA      550
    AGCTCGGTGA TTTGAGGGAT ACGACAACCT CTAAGGCAAT AGCCAGTACT      600
    TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA      650
    ATTAGAGTCT TGGATGGTGA ACAATCAAGT CACTGGTAAT TTACTACGTT      700
25  CAGTATTGCC GGCGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA      750
    TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC      800
    AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC      850
    GAAATGATGC GATTGTTAAA ATTGGTCATT CAATTTTGA CGTTTATACA      900
30  TCACAGTCGC GC                                          912

```

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

2) INFORMATION FOR SEQ ID NO: 1414

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

2) INFORMATION FOR SEQ ID NO: 1415

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

ATGCAGTAAT GCGGCTTTAT C

21

2) INFORMATION FOR SEQ ID NO: 1416

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
(B) STRAIN: HEL-1
(C) ACCESSION NUMBER: X91840

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

	ATGATGAAAA	AATCGTTATG	CTGCGCTCTG	CTGCTGACAG	CCTCTTTCTC	50
	CACATTTGCT	GCCGCAAAAA	CAGAACAAACA	GATTGCCGAT	ATCGTTAATC	100
10	GCACCATCAC	CCCGTTGATG	CAGGAGCAGG	CTATTCCGGG	TATGGCCGTT	150
	GCCGTTATCT	ACCAGGGAAA	ACCCTATTAT	TTCACCTGGG	GTAAAGCCGA	200
	TATCGCCAAT	AACCACCCAG	TCACGCAGCA	AACGCTGTTT	GAGCTAGGAT	250
	CGGTTAGTAA	GACGTTTAAC	GGCGTGTTGG	GCGGCGATGC	TATCGCCCCG	300
	GGCGAAATTA	AGCTCAGCGA	TCCGGTCACG	AAATACTGGC	CAGAACTGAC	350
15	AGGCAAACAG	TGGCAGGGTA	TCCGCCTGCT	GCACTTAGCC	ACCTATACGG	400
	CAGGCGGCCT	ACCGCTGCAG	ATCCCCGATG	ACGTTAGGGA	TAAAGCCGCA	450
	TTACTGCATT	TTTATCAAAA	CTGGCAGCCG	CAATGGACTC	CGGGCGCTAA	500
	GCGACTTTAC	GCTAACTCCA	GCATTGGTCT	GTTTGGCGCG	CTGGCGGTGA	550
	AACCCTCAGG	AATGAGTTAC	GAAGAGGCAA	TGACCAGACG	CGTCCTGCAA	600
20	CCATTAAAC	TGGCGCATAC	CTGGATTACG	GTTCCGCAGA	ACGAACAAAA	650
	AGATTATGCC	TGGGGCTATC	GCGAAGGGAA	GCCCGTACAC	GTTTCTCCGG	700
	GACAACTTGA	CGCCGAAGCC	TATGGCGTGA	AATCCAGCGT	TATTGATATG	750
	GCCCGCTGGG	TTCAGGCCAA	CATGGATGCC	AGCCACGTTC	AGGAGAAAAC	800
	GCTCCAGCAG	GGCATTGCGC	TTGCGCAGTC	TCGCTACTGG	CGTATTGGCG	850
25	ATATGTACCA	GGGATTAGGC	TGGGAGATGC	TGAACTGGCC	GCTGAAAGCT	900
	GATTCGATCA	TCAACGGCAG	CGACAGCAAA	GTGGCATTGG	CAGCGCTTCC	950
	CGCCGTTGAG	GTAAACCCGC	CCGCCCCCGC	AGTGAAAGCC	TCATGGGTGC	1000
	ATAAAACGGG	CTCCACTGGT	GGATTTGGCA	GCTACGTAGC	CTTCGTTCCA	1050
	GAAAAAACC	TTGGCATCGT	GATGCTGGCA	AACAAAAGCT	ATCCTAACCC	1100
30	TGTCCGTGTC	GAGGCGGCCT	GGCGCATTCT	TGAAAAGCTG	CAATAA	1146

2) INFORMATION FOR SEQ ID NO: 1417

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

50 2) INFORMATION FOR SEQ ID NO: 1418

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

10 ATGCTTTACC CAGCGTCAGA TT

22

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTCT CACG

24

2) INFORMATION FOR SEQ ID NO: 1420

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40

TGCTTTACCC AGCGTCAGAT TACG

24

45 2) INFORMATION FOR SEQ ID NO: 1421

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

5

2) INFORMATION FOR SEQ ID NO: 1422

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

20 GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: GRI-1
- (C) ACCESSION NUMBER: X92506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

40

ATGGTTAAAA	AATCACTGCG	TCAGTTCACG	CTGATGGCGA	CGGCAACCGT	50
CACGCTGTTG	TTAGGAAGTG	TGCCGCTGTA	TGCGCAAACG	GCGGACGTAC	100
AGCAAAAAC	TGCCGAATTA	GAGCGGCAGT	CGGGAGGAAG	ACTGGGTGTG	150
GCATTGATTA	ACACAGCAGA	TAATTCGCAA	ATACTTTATC	GTGCTGATGA	200
45 GCGCTTTGCG	ATGTGCAGCA	CCAGTAAAGT	GATGGCCGTG	GCCGCGGTGC	250
TGAAGAAAAG	TGAAAGCGAA	CCGAATCTGT	TAAATCAGCG	AGTTGAGATC	300
AAAAAATCTG	ACTTGGTTAA	CTATAATCCG	ATTGCGGAAA	AGCACGTCGA	350
TGGGACGATG	TCAGTGGCTG	AGCTTAGCGC	GGCCGCGCTA	CAGTACAGCG	400
ATAACGTGGC	GATGAATAAG	CTGATTTCTC	ACGTTGGCGG	CCCGGCTAGC	450
50 GTCACCGCGT	TCGCCCCGACA	GCTGGGAGAC	GAAACGTTCC	GTCTCGACCG	500
TACCGAGCCG	ACGTTAAACA	CCGCCATTCC	GGGCGATCCG	CGTGATACCA	550
CTTCACCTCG	GGCAATGGCG	CAAACCTCTG	GTAATCTGAC	GCTGGGTAAA	600
GCATTGGGTG	ACAGCCAACG	GGCGCAGCTG	GTGACATGGA	TGAAAGGCAA	650

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700
TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750
GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800
CCAGCCTCAA CCTAAGGCAG AAAGCCGTCG CGATGTATTA GCGTCGGCGG 850
5 CTAAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

25 2) INFORMATION FOR SEQ ID NO: 1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

GAATTATCGG CGGTGTTAAT CAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 45 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

CACGCTCAAT ACCGCCATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1427

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

2) INFORMATION FOR SEQ ID NO: 1428

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
(B) STRAIN: CAS-5
(C) ACCESSION NUMBER: X92507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

35	ATGATGACTC AGAGCATTCG CCGCTCAATG TTAACGGTGA TGGCGACGCT	50
	ACCCCTGCTA TTTAGCAGCG CAACGCTGCA TGCGCAGGCG AACAGCGTGC	100
	AACAGCAGCT GGAAGCCCTG GAGAAAAGTT CGGGAGGTCG GCTTGGCGTT	150
	GCGCTGATTA ACACCGCCGA TAATTCGCAG ATTCTCTACC GTGCCGATGA	200
	ACGTTTTGCG ATGTGCAGTA CCAGTAAGGT GATGGCGGCC GCGGCGGTGC	250
	TTAAACAGAG CGAGAGCGAT AAGCACCTGC TAAATCAGCG CGTTGAAATC	300
40	AAGAAGAGCG ACCTGGTTAA CTACAATCCC ATTGCGGAGA AACACGTTAA	350
	CGGCACGATG ACGCTGGCTG AGCTTGGCGC AGCGGCGCTG CAGTATAGCG	400
	ACAATACTGC CATGAATAAG CTGATTGCCC ATCTGGGTGG TCCCGATAAA	450
	GTGACGGCGT TTGCTCGCTC GTTGGGTGAT GAGACCTTCC GTCTGGACAG	500
	AACCGAGCCC ACGCTCAATA CCGCCATTCC AGGCGACCCG CGTGATACCA	550
45	CCACGCCGCT CGCGATGGCG CAGACCCTGA AAAATCTGAC GCTGGGTAAA	600
	GCGCTGGCGG AAATCAGCG GGCACAGTTG GTGACGTGGC TTAAGGGCAA	650
	TACTACCGGT AGCGCGAGCA TTCGGGCGGG TCTGCCGAAA TCATGGGTAG	700
	TGGGCGATAA AACCGGCAGC GGAGATTATG GCACCACCAA CGATATCGCG	750
	GTTATCTGGC CGGAAAACCA CGCACCCTG GTTCTGGTGA CCTACTTTAC	800
50	CCAACCGGAG CAGAAGGCGG AAAGCCGTCG GGATATTCTG GCTGCGGCGG	850
	CGAAAATCGT AACCCACGGT TTCTGA	876

2) INFORMATION FOR SEQ ID NO: 1429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

2) INFORMATION FOR SEQ ID NO: 1430

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAA ACAACCACCG AATAAT

26

2) INFORMATION FOR SEQ ID NO: 1431

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

TAATTGACAC TCCATTTACG GCTAA

25

2) INFORMATION FOR SEQ ID NO: 1432

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

10

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 741 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: AJ223604

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

	ATGAGCAAGT	TATCTGTATT	CTTTATATTT	TTGTTTTGCA	GCATTGCTAC	50
	CGCAGCAGAG	TCTTTGCCAG	ATTTAAAAAT	TGAAAAGCTT	GATGAAGGCG	100
30	TTTATGTTCA	TACTTCGTTT	GAAGAAGTTA	ACGGGTGGGG	CGTTGTTCTT	150
	AAACATGGTT	TGGTGGTTCT	TGTAAATGCT	GAGGCTTACC	TAATTGACAC	200
	TCCATTTACG	GCTAAAGATA	CTGAAAAGTT	AGTCACTTGG	TTTGTGGAGC	250
	GTGGCTATAA	AATAAAAGGC	AGCATTTTCT	CTCATTTTCA	TAGCGACAGC	300
	ACGGGCGGAA	TAGAGTGGCT	TAATTCTCGA	TCTATCCCCA	CGTATGCATC	350
35	TGAATTAACA	AATGAACTGC	TTAAAAAAGA	CGGTAAGGTT	CAAGCCACAA	400
	ATTCATTTAG	CGGAGTTAAC	TATTGGCTAG	TTAAAAATAA	AATTGAAGTT	450
	TTTTATCCAG	GCCCCGGGACA	CACTCCAGAT	AACGTAGTGG	TTTGGTTGCC	500
	TGAAAGGAAA	ATATTATTCG	GTGGTTGTTC	TATTAAACCG	TACGGTTTAG	550
	GCAATTTGGG	TGACGCAAAT	ATAGAAGCTT	GGCCAAAGTC	CGCCAAATTA	600
40	TTAAAGTCCA	AATATGGTAA	GGCAAACCTG	GTTGTTCCAA	GTCACAGTGA	650
	AGTTGGAGAC	GCATCACTCT	TGAAACTTAC	ATTAGAGCAG	GCGGTTAAAG	700
	GGTTAAACGA	AAGTAAAAAA	CCATCAAAAC	CAAGCAACTA	A	741

45

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT

25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG

25

2) INFORMATION FOR SEQ ID NO: 1436

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

35

CAGCATCAAC ATTTAAGATC CCA

24

2) INFORMATION FOR SEQ ID NO: 1437

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGGG AAATTC

26

2) INFORMATION FOR SEQ ID NO: 1438

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: X06046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

```

ATGGCAATCC GAATCTTCGC GATACTTTTC TCCATTTTTT CTCTTGCCAC      50
TTTCGCGCAT GCGCAAGAAG GCACGCTAGA ACGTTCTGAC TGGAGGAAGT      100
TTTTTCAGCGA ATTTCAAGCC AAAGGCACGA TAGTTGTGGC AGACGAACGC      150
CAAGCGGATC GTGCCATGTT GGTTTTGTGAT CCTGTGCGAT CGAAGAAACG      200
CTACTCGCCT GCATCGACAT TCAAGATACC TCATACACTT TTTGCACTTG      250
ATGCAGGCGC TGTTCTGTGAT GAGTTCCAGA TTTTTCGATG GGACGGCGTT      300
AACAGGGGCT TTGCAGGCCA CAATCAAGAC CAAGATTTGC GATCAGCAAT      350
GCGGAATTCT ACTGTTTGGG TGTATGAGCT ATTTGCAAAG GAAATTGGTG      400
ATGACAAAGC TCGGCGCTAT TTGAAGAAAA TCGACTATGG CAACGCCGAT      450
CCTTCGACAA GTAATGGCGA TTAATGGATA GAAGGCAGCC TTGCAATCTC      500
GGCGCAGGAG CAAATTGCAT TTCTCAGGAA GCTCTATCGT AACGAGCTGC      550
CCTTTCGGGT AGAACATCAG CGCTTGGTCA AGGATCTCAT GATTGTGGAA      600
GCCGGTTCGCA ACTGGATACT GCGTGCAAAG ACGGGCTGGG AAGGCCGTAT      650
GGGTTGGTGG GTAGGATGGG TTGAGTGGCC GACTGGCTCC GTATTCTTCG      700
CACTGAATAT TGATACGCCA AACAGAATGG ATGATCTTTT CAAGAGGGAG      750
GCAATCGTGC GGGCAATCCT TCGCTCTATT GAAGCGTTAC CGCCCAACCC      800
GGCAGTCAAC TCGGACGCTG CGCGATAA                                828

```

2) INFORMATION FOR SEQ ID NO: 1439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: J03427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

```

ATGAAAACAT TTGCCGCATA TGTAATTATC GCGTGTCTTT CGAGTACGGC      50

```

	ATTAGCTGGT	TCAATTACAG	AAAATACGTC	TTGGAACAAA	GAGTTCTCTG	100
	CCGAAGCCGT	CAATGGTGTC	TTCGTGCTTT	GTAAAAGTAG	CAGTAAATCC	150
	TGCGCTACCA	ATGACTTAGC	TCGTGCATCA	AAGGAATATC	TTCCAGCATC	200
	AACATTTAAG	ATCCCCAACG	CAATTATCGG	CCTAGAAACT	GGTGTCTATA	250
5	AGAATGAGCA	TCAGGTTTTT	AAATGGGACG	GAAAGCCAAG	AGCCATGAAG	300
	CAATGGGAAA	GAGACTTGAC	CTTAAGAGGG	GCAATACAAG	TTTCAGCTGT	350
	TCCCGTATTT	CAACAAATCG	CCAGAGAAGT	TGGCGAAGTA	AGAATGCAGA	400
	AATACCTTAA	AAAATTTTCC	TATGGCAACC	AGAATATCAG	TGGTGGCATT	450
	GACAAATTCT	GGTTGGAAGG	CCAGCTTAGA	ATTTCGCGAG	TTAATCAAGT	500
10	GGAGTTTCTA	GAGTCTCTAT	ATTTAAATAA	ATTGTCAGCA	TCTAAAGAAA	550
	ACCAGCTAAT	AGTAAAAGAG	GCTTTGGTAA	CGGAGGCGGC	ACCTGAATAT	600
	CTAGTGCATT	CAAAAACCTG	TTTTTCTGGT	GTGGGAACTG	AGTCAAATCC	650
	TGGTGTGCGA	TGGTGGGTTG	GGTGGGTGTA	GAAGGAGACA	GAGGTTTACT	700
	TTTTTCGCCT	TAACATGGAT	ATAGACAACG	AAAGTAAGTT	GCCGCTAAGA	750
15	AAATCCATTC	CCACCAAAAT	CATGGAAAGT	GAGGGCATCA	TTGGTGGCTA	800
	A					801

20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35

2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AACTTTTTTC AGGATC

26

50

2) INFORMATION FOR SEQ ID NO: 1442

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: RNL-1
(C) ACCESSION NUMBER: Z21957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

```
15 ATGAATGTCA TTATAAAAGC TGTAAGTACT GCCTCGACGC TACTGATGGT 50
   ATCTTTTAGT TCATTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC 100
   AAATTGAATC CATAGTCATT GGAAAAAAG CCCTGTAGG CGTTGCAGTG 150
   TGGGGGCCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT 200
20 CCCAATGCAA AGTGTATTTA AATTGCATTT AGCTATGTTG GTACTGCATC 250
   AGGTTGATCA GGGAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG 300
   GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG 350
   AGACGAGTTT AGTGTTCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC 400
   ACAGCGATAA CGTGGCCTGT GATTTGTTAT TTGAACTGGT TGGTGGACCA 450
25 GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT 500
   GGTCGCAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA 550
   ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA 600
   AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT 650
   CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTTA CCAGCTGGTA 700
30 CTGTGGTCGC ACATAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT 750
   GCGGCCACTA ATGATTTAGG TATCATTCTG TTGCCTGATG GACGGCCCTT 800
   GCTGGTTGCT GTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG 850
   AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA 900
   AAGCTTTCTG CCCTAAGCCC AAATTAA 927
35
```

2) INFORMATION FOR SEQ ID NO: 1443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

```
50 CTTCTGCTCT GCTGATGCTT GGC
```

23

2) INFORMATION FOR SEQ ID NO: 1444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTTGTAA TACTGC

26

2) INFORMATION FOR SEQ ID NO: 1445

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: JMC
 (C) ACCESSION NUMBER: X93314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

ATGAATGTCA	TCACAAAATG	TGTTTTTCACC	GCTTCTGCTC	TGCTGATGCT	50
TGGCTTAAGT	TCATTTGTAG	TATCAGCCCA	ATCCCCTTTG	TTAAAAGAGC	100
AGATTGAAAC	CATAGTGACG	GGTAAAAAGG	CCACTGTAGG	TGTAGCAGTG	150
TGGGGGCGCTG	ACGATCTGGA	ACCTTTGTGTG	CTGAATCCAT	TTGAAAAGTT	200
TCCGATGCAA	AGTGTGTTTA	AACTGCATTT	AGCTATGTTA	GTTCTGCATC	250
AGGTCGATCA	GGGGAAACTG	GATTTAAATC	AGTCTGTTC	TGTTAATCGT	300
GCTGCAGTAT	TACAAAATAC	CTGGTCGCCA	ATGATGAAAG	ATCATCAGGG	350
CGATGAATTT	ACTGTTGCAG	TACAGCAGTT	ACTGCAGTAT	TCGGTGTTCAC	400
ACAGCGACAA	TGTGGCCTGC	GATTTGTTAT	TTGAACTGGT	GGGCGGGCCG	450
CAAGCTTTGC	ATGCTTATAT	CCAGTCTTTA	GGCGTTAAAG	AAGCTGCCGT	500
GGTAGCAAAT	GAAGCGCAA	TGCATGCGGA	TGATCAGGTG	CAATATCAAA	550
ACTGGACGTC	GATGAAAGCC	GCAGCACAAG	TTCTGCAAAA	GTTTGAACAG	600
AAAAAGCAGT	TGTCTGAAAC	CTCTCAGGCC	TTGTTATGGA	AATGGATGGT	650
TGAAACCACC	ACAGGACCAC	AGCGGTTAAA	AGGCTTGTTA	CCTGCTGGTA	700
CTATAGTGGC	GCATAAAACC	GGTACTTCGG	GCGTCAGAGC	AGGAAAAACT	750
GCGGCGACTA	ATGATGCGGG	CGTCATTATG	TTGCCTGATG	GACGGCCTTT	800
ATTGGTGGCG	GTATTTGTCA	AGGATTCGGC	TGAATCAGAA	CGAACCAATG	850
AAGCTATTAT	TGCGCAGGTT	GCGCAAGCGG	CTTATCAGTT	TGAGCTGAAA	900
AAACTCTCTG	CAGTGAGTCC	GGATTGA			927

2) INFORMATION FOR SEQ ID NO: 1446

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT

27

2) INFORMATION FOR SEQ ID NO: 1447

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC

23

2) INFORMATION FOR SEQ ID NO: 1448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

GATCAGGTGC ARTATCAAAA CTGGAC

26

2) INFORMATION FOR SEQ ID NO: 1449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

10

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

25

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

40

ATCTACCTGG TCAATCATTG CTTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: BM10393
(C) ACCESSION NUMBER: AF045472

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

10 ATGACATTAT CAATAATTGT CGCTCACGAT AAACAAAGAG TCATTGGGTA 50
CCAAAATCAA TTACCTTGGC ACTTACCAA TGATTTAAG CATATTAAAC 100
AACTGACCAC TGGGAATACA CTTGTAATGG CACGGAAAAC TTTTAATTCT 150
ATAGGGAAGC CATTGCCAAA TAGACGTAAC GTCGTACTCA CTAACCAAGC 200
TTCATTTTAC CATGAAGGGG TAGATGTTAT AAACCTCTCTT GATGAAATTA 250
AAGAGTTATC TGGTCATGTT TTTATATTTG GAGGACAAAC GTTATACGAA 300
GCAATGATTG ACCAGGTAGA TGATATGTAT ATCACAGTAA TAGATGGAAA 350
15 GTTTC AAGGA GACACATTCT TTCCACCATA CACATTCGAA AACTGGGAAG 400
TCGAATCTTC AGTAGAAGGT CAACTAGATG AAAAAAATAC TATACCGCAT 450
ACATTCTTAC ATTTAGTGCG TAGAAAAGGG AAATAG 486

20

2) INFORMATION FOR SEQ ID NO: 1453

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

ATCGAAGAAT GGAGTTATCG GRAATG

26

35

2) INFORMATION FOR SEQ ID NO: 1454

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

CCTAAAAYTR CTGGGGATTT CWGGA

25

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2) INFORMATION FOR SEQ ID NO: 1455

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455

CAGGTGGTGG GGAGATATAC AAAA

24

2) INFORMATION FOR SEQ ID NO: 1456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456

TATGTTAGAS RCGAAGTCTT GGKTAA

26

2) INFORMATION FOR SEQ ID NO: 1457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457

CAAAGGTGAA CAGCTCCTGT TT

22

2) INFORMATION FOR SEQ ID NO: 1458

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GCTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

5
GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA 50
TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG 100
CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA 150
ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT 200
10 TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT 250
TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG 300
GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC 350
AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA 400
ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT 450
15 TACCAAATCT GGCAAAGGG TTAA 474

2) INFORMATION FOR SEQ ID NO: 1462

20
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

30
GCACTCCCYA ATAGGAAATA CGC 23

35 2) INFORMATION FOR SEQ ID NO: 1463

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

AGTGTTGCTC AAAAACAAC TCG 23

50
2) INFORMATION FOR SEQ ID NO: 1464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

30 2) INFORMATION FOR SEQ ID NO: 1466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

AAGCATTGAC CTACAATCAG TGT

23

45

2) INFORMATION FOR SEQ ID NO: 1467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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